

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 5, 2003, 14:26:38 ; Search time 35.3599 Seconds  
(without alignments)  
3196.087 Million cell updates/sec

Title: US-09-854-356-7

Perfect score: 3954

Sequence: 1 MELAALCRWGLLALLPPCA.....GFFCPDPAPGAGMVHRRH 712

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A. Geneseq 15Jun03.\*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
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- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
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- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3954	100.0	712	21	Human HER-2/neu fu
2	3954	100.0	712	23	Her-2/neu extracel
3	3954	100.0	919	21	Human HER-2/neu fu
4	3954	100.0	919	23	Her-2/neu extracel
5	3776	95.5	1200	21	Human HER-2/neu pr
6	3776	95.5	1255	17	HER-2/neu protein.
7	3776	95.5	1255	21	Human HER-2/neu on
8	3776	95.5	1255	21	Human HER-2/neu pr
9	3776	95.5	1255	21	Amino acid sequenc

10	3776	95.5	1255	21	AA192620	Human heregulin 2
11	3776	95.5	1255	22	AAE12130	Human tyrosine kin
12	3776	95.5	1255	22	AAE12130	Human HER-2/neu pr
13	3776	95.5	1255	22	AAE12130	HER2/neu amino aci
14	3776	95.5	1255	22	AAE12130	HER2 transgene pla
15	3776	95.5	1255	23	AAE12130	Human HER-2 protei
16	3776	95.5	1255	23	AAE12130	Human HER2 antigen
17	3776	95.5	1255	23	AAE12130	Human Her-2/neu pr
18	3776	95.5	1255	23	AAE12130	Human Her-2/neu pr
19	3776	95.5	1255	23	AAE12130	Human Her-2/neu on
20	3776	95.5	1255	23	AAU77114	Human HER-2 (erbB2)
21	3776	95.5	1255	23	AAU77114	Breast cancer asso
22	3776	95.5	1255	24	ABR47447	Human Her2/Neu pro
23	3776	95.5	1255	24	ABP74708	Sequence of c-erbB
24	3776	95.5	1255	24	AAE12130	Her2-GM-CSF immuno
25	3632	91.9	782	18	AAW19764	Extracellular HER-
26	3628	91.8	653	21	AAE12130	Human HER-2/neu on
27	3628	91.8	653	23	AAE12130	Human breast cance
28	3606	91.2	1223	23	AAE12130	Human erbB2 oncopr
29	3590	90.8	645	22	AAE12130	Human erbB2 extrac
30	3590	90.8	645	22	AAE12130	Human HER2 recepto
31	3590	90.8	645	23	ABG70753	DC8scFv-erbB2EC fu
32	3525	89.2	951	21	AAE12130	Extracellular port
33	3422	86.5	624	11	AAE12130	Mouse Her-2/neu ex
34	3373.5	85.3	920	23	AAE12130	Mouse Her-2/neu ex
35	3373.5	85.3	926	23	AAE12130	Rat HER-2/neu prot
36	3209.5	81.2	1256	21	AAE12130	Rat Her-2/neu onco
37	3209.5	81.2	1256	23	AAE12130	Mouse Her-2/neu pr
38	3189.5	80.7	1256	21	AAE12130	Amino acid sequenc
39	3189.5	80.7	1256	22	AAE12130	Mouse Her-2/neu on
40	3189.5	80.7	1256	23	AAE12130	Rat HER-2/neu prot
41	3110.5	78.7	654	21	AAE12130	Rat Her-2/neu onco
42	3110.5	78.7	654	23	AAE12130	Truncated HER-2, p
43	1827	46.2	420	21	AAE12130	Human p68HER-2 gen
44	1825.5	46.2	419	22	AAE12130	Human truncated HE
45	1824.5	46.1	419	23	AAE12130	

ALIGNMENTS

RESULT 1	
AAE12130	
ID	AAE12130 standard; protein; 712 AA.
XX	
AC	AAE12130;
XX	
DT	12-JAN-2001 (first entry)
XX	
DE	Human HER-2/neu fusion protein.
XX	
KW	Human; HER-2/neu; oncogene; tyrosine kinase; cytotstatic; vaccine;
KW	Breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW	colon cancer; fusion protein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FN	WO200044899-A1.
XX	
PD	03-AUG-2000.
XX	
PF	28-JAN-2000; 2000WO-US02164.
XX	
PR	29-JAN-1999; 99US-0117976.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	(SMIK) SMITHKLINE BEECHAM.
XX	
PI	Cheever MA, Chaysen D;
XX	
DR	WPI; 2000-505976/45.
XX	

HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
 PT useful for vaccinating against breast, ovarian, colon, lung and  
 prostate cancers -

Claim 27; Fig 13; 128pp; English.

The present sequence is a fusion protein comprising the extracellular  
 domain and a preferred portion of the phosphorylation domain of the human  
 HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of  
 receptor-like glycoproteins and shows homology to the epidermal growth  
 factor receptor (EGFR). It probably plays a part in cell growth and/or  
 differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion  
 proteins may be used to treat or prevent cancer by eliciting or enhancing  
 an immune response to the HER-2/neu protein. They may be used to treat  
 malignancies such as breast, ovarian, colon, lung and prostate cancers,  
 and may be used as an antigen to vaccinate against these neoplasias.

XX Sequence 712 AA;

Query Match 100.0%; Score 3954; DB 21; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-299;  
 Matches 712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAALCRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMLRHLYQGCVVQGNL 60  
 DB 1 MELAALCRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMLRHLYQGCVVQGNL 60

QY 61 ELYLPTNASLSFLQDIOEQVGVLAHNOVROVPLQRLIRVGTQOLFEDNALAVLDNG 120  
 DB 61 ELYLPTNASLSFLQDIOEQVGVLAHNOVROVPLQRLIRVGTQOLFEDNALAVLDNG 120

QY 121 DPLNNTPTVGTGASPGGLREQLRLSTEILKGGVLIQRNPOLCYQDTILWKDIFHKNQLA 180  
 DB 121 DPLNNTPTVGTGASPGGLREQLRLSTEILKGGVLIQRNPOLCYQDTILWKDIFHKNQLA 180

QY 181 LTLIDNTRGRACHPCSPMKGSRCSWESSEDCOSLRTVTCAGCARCKGPLPTDCHEQC 240  
 DB 181 LTLIDNTRGRACHPCSPMKGSRCSWESSEDCOSLRTVTCAGCARCKGPLPTDCHEQC 240

QY 241 AGCTGPKGSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPGRYTFGASCVTACP 300  
 DB 241 AGCTGPKGSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPGRYTFGASCVTACP 300

QY 301 YNYLSTDVGSCTLVCPHNOEVTAEADGTORCEKSCPKARVCYGLGWEHLREVRVTSAN 360  
 DB 301 YNYLSTDVGSCTLVCPHNOEVTAEADGTORCEKSCPKARVCYGLGWEHLREVRVTSAN 360

QY 361 IQEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQEQVFTLEITGYLYISAWPDSLP 420  
 DB 361 IQEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQEQVFTLEITGYLYISAWPDSLP 420

QY 421 DLSVFQNLQVIRGRIILHNGAYSTLQGLGISWLGSLRELGSGLALIHNTHLCFVHTV 480  
 DB 421 DLSVFQNLQVIRGRIILHNGAYSTLQGLGISWLGSLRELGSGLALIHNTHLCFVHTV 480

QY 481 PWDQLFRNPHOALLHTANRPEDECVCEGLACHOLCARGHCWGPGPTQVCNCSOFLRGQEC 540  
 DB 481 PWDQLFRNPHOALLHTANRPEDECVCEGLACHOLCARGHCWGPGPTQVCNCSOFLRGQEC 540

QY 541 VEECRVLQGLPREYVYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKPPFCVARC 600  
 DB 541 VEECRVLQGLPREYVYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKPPFCVARC 600

QY 601 PSQVKEPDLSPYMTKPFDEBAGACPCINCTHSCVDLDKGCFAORASPLTSQNEDLGP 660  
 DB 601 PSQVKEPDLSPYMTKPFDEBAGACPCINCTHSCVDLDKGCFAORASPLTSQNEDLGP 660

QY 661 ASPLDSTFYRSLLEDDMGDLVDAEYLYVPQQGFFCDDPAPGAGGMVHRRH 712  
 DB 661 ASPLDSTFYRSLLEDDMGDLVDAEYLYVPQQGFFCDDPAPGAGGMVHRRH 712

AAW51149  
 ID AAW51149 standard; Protein; 712 AA.  
 XX  
 AC AAW51149;  
 XX  
 DT 17-JUN-2002 (first entry)  
 XX  
 DE Her-2/neu extracellular domain-delta-phosphorylation domain fusion.  
 KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..653  
 FT Domain /note= "extracellular domain"  
 FT Domain 654..712  
 FT Domain /note= "phosphorylation domain fragment"

WO200212341-A2.  
 14-FEB-2002.  
 03-AUG-2001; 2001WO-US24283.  
 03-AUG-2000; 2000US-0632507.  
 (CORI-) CORIXA CORP.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Cheever MA, Gheysen D;  
 DR WPI; 2002-241743/29.  
 XX  
 PT Her-2/neu fusion protein for treating or preventing cancer by eliciting  
 PT or enhancing an immune response to the protein, has Her-2/neu  
 PT extracellular domain fused to Her-2/neu intracellular or  
 PT phosphorylation domain -  
 XX  
 PS Claim 37; Fig 13; 141pp; English.  
 XX  
 CC The present sequence is that of a fusion protein between the  
 CC extracellular domain and a fragment (DeltapD) of the phosphorylation  
 CC domain of human Her-2/neu (see AAW51143), an oncogenic self-protein  
 CC and target for anti-cancer vaccines. The fusion protein can be  
 CC obtained by recombinant DNA methods. Her-2/neu overexpression  
 CC correlates with a poor prognosis in breast and ovarian cancers.  
 CC The invention provides Her-2/neu fusion proteins, nucleic acids  
 CC encoding them, viral vectors, and vaccines comprising the fusion  
 CC proteins or nucleic acid molecules. In preferred fusion proteins,  
 CC the extracellular domain of Her-2/neu is fused to a Her-2/neu  
 CC intracellular domain or phosphorylation domain (or its DeltapD  
 CC fragment). An immune response to Her-2/neu protein is elicited or  
 CC enhanced by administering the fusion protein in the form of a vaccine,  
 CC or by transfecting cells of an animal ex vivo with a nucleic acid  
 CC encoding the fusion protein, and delivering the transfected cells  
 CC to the animal. The fusion proteins, nucleic acids, and isolated  
 CC specific T-cells are useful for inhibiting the development of a  
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer  
 CC in a patient. T cells that specifically react with a Her-2/neu  
 CC fusion protein can be used to remove tumour cells from a sample in  
 CC order to inhibit the development of cancer in a patient.

XX  
 SQ Sequence 712 AA;

Query Match 100.0%; Score 3954; DB 23; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-299;  
 Matches 712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MELAALCRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMLRHLYQGCVVQGNL 60

QY 61 ELTYLPTNASLSFLQDIOEVQGVLIHNVQVPLQRLRIVRGTQLPEDNVALAVLNG 120  
 DB |||||  
 QY 61 ELTYLPTNASLSFLQDIOEVQGVLIHNVQVPLQRLRIVRGTQLPEDNVALAVLNG 120  
 DB |||||  
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 DB |||||  
 QY 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGVLIQVLPOLCYQDTILWKDIFHKNNQLA 180  
 DB |||||  
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 DB |||||  
 QY 181 LTLIDTNSRACHPCSPMKGRSGESSEDCQSLTRTVACGACRCKGPLETDCCHQC 240  
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 QY 421 DLSVFQNLQVIRGRILHNGAYSLTLQGLISWGLRLSRLSRELGLALIHNTLHLCFVHTV 480  
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 DB |||||  
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## RESULT 3

ID AAB21203  
 AC AAB21203 standard; protein; 919 AA.

XX AAB21203;  
 XX

DT 12-JAN-2001 (first entry)

DE Human HER-2/neu fusion protein.

KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;  
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;  
 KW colon cancer; fusion protein.

XX Homo sapiens.

OS Synthetic.

XX WO200044899-A1.

PN 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US02164.

XX 29-JAN-1999; 99US-0117976.

XX (CORI-) CORIXA CORP.

PA (SMIK) SMITHKLINE BEECHAM.

XX Cheever MA, Gheysen D;  
 XX WPI; 2000-505976/45.

XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
 PT useful for vaccinating against breast, ovarian, colon, lung and  
 PT prostate cancers -

XX Claim 2; Fig 12; 128pp; English.

XX The present sequence is a fusion protein comprising the extracellular  
 CC domain and the phosphorylation domain of the human HER-2/neu protein.  
 CC HER-2/neu is a member of the tyrosine kinase family of receptor-like  
 CC glycoproteins and shows homology to the epidermal growth factor receptor  
 CC (EGFR). It probably plays a part in cell growth and/or differentiation.  
 CC The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used  
 CC to treat or prevent cancer by eliciting or enhancing an immune response  
 CC to the HER-2/neu protein. They may be used to treat malignancies such as  
 CC breast, ovarian, colon, lung and prostate cancers, and may be used as an  
 CC antigen to vaccinate against these neoplasias.

XX Sequence 919 AA;

Query Match 100.0%; Score 3954; DB 21; Length 919;

Best Local Similarity 100.0%; Pred. No. 6e-299;

Matches 712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAALCWGILLALLPFGAASQVCTGTDKMLRLPASPEHLDMLRHLQSCQVQGNL 60

DB |||||

QY 1 MELAALCWGILLALLPFGAASQVCTGTDKMLRLPASPEHLDMLRHLQSCQVQGNL 60

DB |||||

QY 61 ELTYLPTNASLSFLQDIOEVQGVLIHNVQVPLQRLRIVRGTQLPEDNVALAVLNG 120

DB |||||

QY 61 ELTYLPTNASLSFLQDIOEVQGVLIHNVQVPLQRLRIVRGTQLPEDNVALAVLNG 120

DB |||||

QY 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGVLIQVLPOLCYQDTILWKDIFHKNNQLA 180

DB |||||

QY 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGVLIQVLPOLCYQDTILWKDIFHKNNQLA 180

DB |||||

QY 181 LTLIDTNSRACHPCSPMKGRSGESSEDCQSLTRTVACGACRCKGPLETDCCHQC 240

DB |||||

QY 181 LTLIDTNSRACHPCSPMKGRSGESSEDCQSLTRTVACGACRCKGPLETDCCHQC 240

DB |||||

QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300

DB |||||

QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300

DB |||||

QY 301 YNYLSTDVGSCTLVCPHNSQVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360

DB |||||

QY 301 YNYLSTDVGSCTLVCPHNSQVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360

DB |||||

QY 361 IOEFAGCKKIFGSLAPLPSFPGDPAASNTAPLOPQLOVFETLEETGYLYISAWPDSL 420

DB |||||

QY 361 IOEFAGCKKIFGSLAPLPSFPGDPAASNTAPLOPQLOVFETLEETGYLYISAWPDSL 420

DB |||||

QY 421 DLSVFQNLQVIRGRILHNGAYSLTLQGLISWGLRLSRLSRELGLALIHNTLHLCFVHTV 480

DB |||||

QY 421 DLSVFQNLQVIRGRILHNGAYSLTLQGLISWGLRLSRLSRELGLALIHNTLHLCFVHTV 480

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QY 481 PWDQLFRNPHQALLHTANRPEDECYVGEGLACHOLCARGCWGPGPTQCVNCSQFLRGQEC 540

DB |||||

QY 481 PWDQLFRNPHQALLHTANRPEDECYVGEGLACHOLCARGCWGPGPTQCVNCSQFLRGQEC 540

DB |||||

QY 541 VVECRVLOGLPREYVNAHCLPCHPECPONGSVTCFGEADOCVACAHYKDPPEFCVAC 600

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QY 541 VVECRVLOGLPREYVNAHCLPCHPECPONGSVTCFGEADOCVACAHYKDPPEFCVAC 600

DB |||||

QY 601 PSGVKPDLISYMPIWKFPDEEGACQPCINCHTSCVDLDDKGCPCAEORASPLTSQNEIDLGP 660

DB |||||

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DB |||||

QY 661 ASPLDSTFYRSLLEDDMDGLVDAEYLVPOQGFPCDPAPGAGGMVHHRH 712



```
PR 29-JAN-1999; 99US-0117976.
XX (CORI-) CORIXA CORP.
PA (SMIK ) SMITHKLINE BEECHAM.
XX
XX Cheever MA, Gheysen D;
XX WPI; 2000-505976/45.
DR N-PSDB; AAA89736.
XX
XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT useful for vaccinating against breast, ovarian, colon, lung and
PT prostate cancers -
XX
XX Disclosure; Fig 15; 128pp; English.
XX
XX The present sequence is the human HER-2/neu protein. It is a member
CC of the tyrosine kinase family of receptor-like glycoproteins and shows
CC homology to the epidermal growth factor receptor (EGFR). It probably
CC plays a part in cell growth and/or differentiation. The HER-2/neu
CC gene is an oncogene. An HER-2/neu fusion protein comprising a
CC HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation
CC domain may be used to treat or prevent cancer by eliciting or
CC enhancing an immune response to the HER-2/neu protein. It may be used
CC to treat malignancies such as breast, ovarian, colon, lung and
CC prostate cancers, and may be used as an antigen to vaccinate against
CC these neoplasias.
XX
XX Sequence 1200 AA;
XX
XX Query Match 95.5%; Score 3776; DB 21; Length 1200;
XX Best Local Similarity 67.9%; Pred. No. 6.2e-285;
XX Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;
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DB 1 MELALCNRWGLLLALPPGAASQVCTGDMKRLPASPETHLDMRLHYQCQVQGNL 60
QY 61 ELTYLPTNASLFLQDIOEVQGVYLIHNRQVPLQRLIRVRGTLFEDNVALAVLNG 120
DB 61 ELTYLPTNASLFLQDIOEVQGVYLIHNRQVPLQRLIRVRGTLFEDNVALAVLNG 120
QY 121 DPLNNTPTVGTASPGGLREQLRSLEILKGGVLQIQRNPOLCYQDTILWKDIFHKNNQLA 180
DB 121 DPLNNTPTVGTASPGGLREQLRSLEILKGGVLQIQRNPOLCYQDTILWKDIFHKNNQLA 180
QY 181 LTLIDTNRSRACHPCSPMCKSGRCWGESSEDCQSLTRTVCCAGCARCKGPLPTDCCHQC 240
DB 181 LTLIDTNRSRACHPCSPMCKSGRCWGESSEDCQSLTRTVCCAGCARCKGPLPTDCCHQC 240
QY 241 AAGCTGPKHSDCLACLFHNHSGICELHCPALVTYNTDTFESMPNPEGRYTGASCVTACP 300
DB 241 AAGCTGPKHSDCLACLFHNHSGICELHCPALVTYNTDTFESMPNPEGRYTGASCVTACP 300
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRVTSAN 360
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRVTSAN 360
QY 361 IOEFAGCKKIFGSLAFLESFPGDPSANTAPLOPEQLQVFETLEITGYLYISAWPDSLP 420
DB 361 IOEFAGCKKIFGSLAFLESFPGDPSANTAPLOPEQLQVFETLEITGYLYISAWPDSLP 420
QY 421 DLSVFQNLQVIRGRLTHNGAVSLTQGLIGISWLGRLSRLGSLALTHNTHLCFVHTV 480
DB 421 DLSVFQNLQVIRGRLTHNGAVSLTQGLIGISWLGRLSRLGSLALTHNTHLCFVHTV 480
QY 481 PWDQLFRNPHQALLHTANRPEDECVEGLACHOLCARGHCWGPPTQCVCNSQFLRGQEC 540
DB 481 PWDQLFRNPHQALLHTANRPEDECVEGLACHOLCARGHCWGPPTQCVCNSQFLRGQEC 540
QY 541 VEECRVLQGLPREYNARHCLPCHPECPQNGSVTFCFGEADQCACAHYKDPDFCVARC 600
DB 541 VEECRVLQGLPREYNARHCLPCHPECPQNGSVTFCFGEADQCACAHYKDPDFCVARC 600
```

```
QY 601 PSQVKPDLSTYMPIWKFPDEGACQPCPINCTHSCVDLDDKGCQPAEQRASPLTS 653
DB 601 PSQVKPDLSTYMPIWKFPDEGACQPCPINCTHSCVDLDDKGCQPAEQRASPLTSIIISAVVG 660
XX
QY 654 ----- 653
DB 661 ILLVVVLGVWFVGIILKRRQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720
XX
QY 654 ----- 653
DB 721 RKVKVLSGAPGTYYKGIWIPDGENVKIPVAIKVLRNTSPKANKEILDEAYVMAGVSP 780
XX
QY 654 ----- 653
DB 781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRLGSLQDLLNWCMDIAKGMSYLEVDVR 840
XX
QY 654 ----- 653
DB 841 LVHRDLAARNVLVKSNNHVKITDFGLARLLDIDETEHADGGKVPKWMALLESILRRRFT 900
XX
QY 654 ----- 653
DB 901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICITIDYVIMVWKWM 960
XX
QY 654 -----QNEDLGPASPLDSTFYRSLLDEDDMGDLVDA 684
DB 961 IDSECRPRFRELVSERFMRDPPQRFVVIQNEDLGPASPLDSTFYRSLLDEDDMGDLVDA 1020
XX
QY 685 BEYLVPQOGFFCPDPAPGAGGMVHHRH 712
DB 1021 BEYLVPQOGFFCPDPAPGAGGMVHHRH 1048
XX
XX AAW01111;
XX
DT 01-JAN-1997 (first entry)
XX
DE HER-2/neu protein.
XX
KW HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;
KW breast cancer; ovary cancer; colon cancer; lung cancer;
KW prostate cancer; immunisation; tumour; vaccine; vector.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 676..1255
XX FT /label= intracellular_domain
XX FT /note= "claimed domain, useful for immunisation"
XX
XX WO9630514-A1.
XX
XX 03-OCT-1996.
XX
XX 28-MAR-1996; 96WO-US01689.
XX
XX 31-MAR-1995; 95US-0414417.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Cheever MA, Disis ML;
XX
XX WPI; 1996-455361/45.
XX
XX N-PSDB; AAT40739.
XX
XX DNA encoding HER-2-neu poly:peptide(s) - used for prevention or
XX treatment of malignancies with which the HER-2/neu oncogene is
XX associated
```

XX PS  
XX PS  
CC Claim 2; Page 56-61; 71pp; English.  
CC Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is  
CC the product of the HER-2/neu oncogene (see also AAT40739). The  
CC protein is over-expressed in various cancers, including breast,  
CC ovarian, colon, lung and prostate. The intracellular domain of the  
CC protein can be used to immunise an animal against a malignancy with  
CC which the oncogene is associated. The polypeptide can be produced  
CC in transformed host cells for use in immunisation. Alternatively,  
CC animal cells are transfected in vivo or ex vivo with a viral vector  
CC that directs expression of the polypeptide.  
XX Sequence 1255 AA;  
XX Query Match 95.5%; Score 3776; DB 17; Length 1255;  
XX Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
XX Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
XX  
QY 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMLRHLRYQCQVQGNL 60  
DB 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMLRHLRYQCQVQGNL 60  
QY 61 ELTYLPTNASLFLQDIQEVQGVLIHAHQVQVPLQRLIRVGTQLFEDNYVALVLDNG 120  
DB 61 ELTYLPTNASLFLQDIQEVQGVLIHAHQVQVPLQRLIRVGTQLFEDNYVALVLDNG 120  
QY 121 DPLNNTPTVGTASPGGLRLQLRLSLTEILKGGVLIQPNPOLCYODTILWKDIFHKNOLA 180  
DB 121 DPLNNTPTVGTASPGGLRLQLRLSLTEILKGGVLIQPNPOLCYODTILWKDIFHKNOLA 180  
QY 181 LTLIDNRRACHPCSPCKGSRGWESSEDQSLTRTVAGGCARCKGPLEPTDCHEOC 240  
DB 181 LTLIDNRRACHPCSPCKGSRGWESSEDQSLTRTVAGGCARCKGPLEPTDCHEOC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGCASCVTAC 300  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGCASCVTAC 300  
QY 301 YNLSLTDVGSCTLVCPHLNQVTAEDGTQCEKSCPCARVCYGLGMEHLREVRAVTSAN 360  
DB 301 YNLSLTDVGSCTLVCPHLNQVTAEDGTQCEKSCPCARVCYGLGMEHLREVRAVTSAN 360  
QY 361 IQEFACKIIFGSLAFIPSGFDGPNASNTAPLOEQLOVFETLEETGYLYISAMPDLSLP 420  
DB 361 IQEFACKIIFGSLAFIPSGFDGPNASNTAPLOEQLOVFETLEETGYLYISAMPDLSLP 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGSIWGLSLRELGLALIHNTHLCPVHTV 480  
DB 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGSIWGLSLRELGLALIHNTHLCPVHTV 480  
QY 481 PWDQFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPPTQCVNCSQFLRGQBC 540  
DB 481 PWDQFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPPTQCVNCSQFLRGQBC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPCOPONGSVTCFGEADOCVACHYKPPFCVARG 600  
DB 541 VEECRVLQGLPREYVNAHCLPCHPCOPONGSVTCFGEADOCVACHYKPPFCVARG 600  
QY 601 PSQVKPDLSPYMPWKPFDEBAGACQPCINCTHSCVDLDDKGCFAEQRASPLTS 653  
DB 601 PSQVKPDLSPYMPWKPFDEBAGACQPCINCTHSCVDLDDKGCFAEQRASPLTS 653  
QY 654  
DB 661 ILLVVLGVVFGILIKRQKIRKTYMRLLOETELVEPLTPSGAMPNQAQMRILKETEL 720  
QY 654  
DB 721 RKVKVLGSGAGFVYGIWIPDGNVKIPVAIKVLRNTSPKANKILDEAYVMAGVGSF 780  
QY 654

DB 781 YVSRLLGICLTSTVQLVLTQMPYGCGLLDHVRENRGLSGQDLLNWCMIKMSYLEVDR 840  
QY 654  
DB 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKGVPIKWWALESILRERFT 900  
QY 654  
DB 901 HQSDVMSYGVTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPPICITIDVYIMVIMVCKWM 960  
QY 654  
DB 961 IDSECRPRFRLVSEFSEMRARDPQRFVVIQNEGLGPASPLDSTFYRSLEDDDDMGDLVDA 1020  
QY 685 EBYLVPQOGFFCPDPAPGAGGVMVHRHR 712  
DB 1021 EBYLVPQOGFFCPDPAPGAGGVMVHRHR 1048  
XX  
XX AC AAW92406; Protein; 1255 AA.  
XX DT 21-APR-1999 (first entry)  
XX DE Human HER-2/neu oncogene protein.  
XX KW HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;  
XX OS malignancy; treatment; tumour.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Region 676..1255  
XX FT /note= "region which elicits immune response"  
XX PN US5869445-A.  
XX PD 09-FEB-1999.  
XX PF 01-APR-1996; 96US-0625101.  
XX PR 01-APR-1996; 96US-0625101.  
XX PR 17-MAR-1993; 93US-0033644.  
XX PR 12-AUG-1993; 93US-0106112.  
XX PR 31-MAR-1995; 95US-0414417.  
XX (UNIW ) UNIV WASHINGTON.  
XX PI Cheever MA, Disis ML;  
XX WPI; 1999-152835/13.  
XX N-PSDB; AAX01912.  
XX Use of HER-2/neu polypeptides - for eliciting an immune response to  
XX an HER-2/neu associated malignancy, particularly for treating or  
XX preventing tumours  
XX Claim 3; Column 31-38; 26pp; English.  
XX CC This sequence represents the human HER-2/neu oncogene protein. A fragment  
XX of this protein is used in a method for eliciting or enhancing an immune  
XX response to HER-2/neu protein. The polypeptide can stimulate T cells and  
XX B cells to produce an immune response to the HER-2/neu protein. The  
XX method can be used for immunisation against a malignancy in which the  
XX HER-2/neu oncogene is associated and in the treatment of an existing  
XX tumour, or to prevent tumour occurrence or reoccurrence.  
XX Sequence 1255 AA;  
XX Query Match 95.5%; Score 3776; DB 20; Length 1255;

Best Local Similarity 67.9%; Pred. No. 6,6e-285;		Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;	
QY	1	MELAAACRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMRLHLYQCQVQGNL	60
Db	1	MELAAACRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMRLHLYQCQVQGNL	60
QY	61	ELTYLPTNASLFLQDIQEVQGVLIHNVQVPLQRLRIVRGTLFEDNYALAVLNG	120
Db	61	ELTYLPTNASLFLQDIQEVQGVLIHNVQVPLQRLRIVRGTLFEDNYALAVLNG	120
QY	121	DPLNNTTPTVGTASPGGLRELQRLSRLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
Db	121	DPLNNTTPTVGTASPGGLRELQRLSRLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
QY	181	LTLIDTNRSRACHPCS PMCKGSRGWESSEDCQSITRTVCAGGCARCKGPLEPTDCCHQC	240
Db	181	LTLIDTNRSRACHPCS PMCKGSRGWESSEDCQSITRTVCAGGCARCKGPLEPTDCCHQC	240
QY	241	AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP	300
Db	241	AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP	300
QY	301	YNYLSTDVGSCTLVCPHNSQVTAEDGTQRCCKSPCARVCYGLGMEHLRVRVAVTSAN	360
Db	301	YNYLSTDVGSCTLVCPHNSQVTAEDGTQRCCKSPCARVCYGLGMEHLRVRVAVTSAN	360
QY	361	IOEFAGCKKIFGSLAFPLSPFSGDPSANTAPLOPEQLQVFETLEITGYLISAMPDLSL	420
Db	361	IOEFAGCKKIFGSLAFPLSPFSGDPSANTAPLOPEQLQVFETLEITGYLISAMPDLSL	420
QY	421	DLVSFQNLQVIRGRILHNGAYSLTLQGLGISWGLSRLSRELGLALIHNTLHLCFVHTV	480
Db	421	DLVSFQNLQVIRGRILHNGAYSLTLQGLGISWGLSRLSRELGLALIHNTLHLCFVHTV	480
QY	481	PWDQLFRNPHQALLHTANRPEDECVEGLACHOLCARGHGWPGTQCVCNCSQFIRGQEC	540
Db	481	PWDQLFRNPHQALLHTANRPEDECVEGLACHOLCARGHGWPGTQCVCNCSQFIRGQEC	540
QY	541	VEECVVLQGLPREYNARHCLPCHPECPONGSVTCFGEADQCVACAHYKDPPECVAC	600
Db	541	VEECVVLQGLPREYNARHCLPCHPECPONGSVTCFGEADQCVACAHYKDPPECVAC	600
QY	601	PSGVKPDLSYMIWKFPEDEGACQPCINCHTSCVDLDDKGCAPQASPLTS	653
Db	601	PSGVKPDLSYMIWKFPEDEGACQPCINCHTSCVDLDDKGCAPQASPLTS	653
QY	654	-----	653
Db	661	ILLVVLGVVFGILIKRQOKIRKVTMRLLQETELVEPLTPSGAMPNQAQMRILKETEL	720
QY	654	-----	653
Db	721	RKVKVLGSGAFVTVYGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVSP	780
QY	654	-----	653
Db	781	YVSRLLIGICTSTVQLVTQMLPYGCLLDHVRNENRGLSGODLLNMCQIAKMSYLEDR	840
QY	654	-----	653
Db	841	LVRDLAARNVLKSPNHVKITDGLARLLDIDETEYHADGKVPKIKWMALESILRRFT	900
QY	654	-----	653
Db	901	HOSDVMSYGVTVWELMTFGAKPYDGPAREIPDLLEKGERLPQPPICTIDVTYIMVKWM	960
QY	654	-----	653
Db	961	INSECRPRFRELVSFSEMRARDPQFVVIQNEEDLGPASPLDSTFYRSLEDDMDGLVDA	1020
QY	685	BEYLVPOQGFPCDPAPGAGGMVHHRH 712	

Db	1021	BEYLVPOQGFPCDPAPGAGGMVHHRH 1048	
RESULT 8			
AAE21198			
ID	AAE21198	standard; protein; 1255 AA.	
XX			
AC	AAE21198;		
DT	12-JAN-2001	(first entry)	
XX			
DE	Human HER-2/neu protein.		
XX			
KW	Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;		
KW	breast cancer; prostate cancer; ovarian cancer; lung cancer;		
KW	colon cancer.		
XX	Homo sapiens.		
XX	WO200044899-A1.		
PN	03-AUG-2000.		
PD			
XX			
PF	28-JAN-2000; 2000WO-US02164.		
XX			
PR	29-JAN-1999; 99US-0117976.		
XX			
PA	(CORI-) CORIXA CORP.		
PA	(SMIK) SMITHKLINE BEECHAM.		
XX			
PI	Cheever MA, Gheysen D;		
XX			
DR	WPI; 2000-505976/45.		
DR	N-PSDB; AAA89736.		
XX			
PT	HER-2/neu extracellular domain/phosphorylation domain fusion proteins		
PT	useful for vaccinating against breast, ovarian, colon, lung and		
PT	prostate cancers -		
XX			
PS	Claim 52; Fig 7; 128pp; English.		
XX			
CC	The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias.		
XX			
SQ	Sequence 1255 AA;		
Query Match 95.5%; Score 3776; DB 21; Length 1255;			
Best Local Similarity 67.9%; Pred. No. 6,6e-285;			
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;			
QY	1	MELAAACRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMRLHLYQCQVQGNL	60
Db	1	MELAAACRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMRLHLYQCQVQGNL	60
QY	61	ELTYLPTNASLFLQDIQEVQGVLIHNVQVPLQRLRIVRGTLFEDNYALAVLNG	120
Db	61	ELTYLPTNASLFLQDIQEVQGVLIHNVQVPLQRLRIVRGTLFEDNYALAVLNG	120
QY	121	DPLNNTTPTVGTASPGGLRELQRLSRLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
Db	121	DPLNNTTPTVGTASPGGLRELQRLSRLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
QY	181	LTLIDTNRSRACHPCS PMCKGSRGWESSEDCQSITRTVCAGGCARCKGPLEPTDCCHQC	240



Db 181 LTLIDTNRSRACHPCSPMCKGSRGSESSDCQSLTRTVACGACRCKGPLPTDCCHEQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 QY 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFFETLEETGYLYISAWPDSL 420  
 Db 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFFETLEETGYLYISAWPDSL 420  
 QY 421 DLSVFONLQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNNHLCFVHTV 480  
 Db 421 DLSVFONLQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNNHLCFVHTV 480  
 QY 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQBC 540  
 Db 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQBC 540  
 QY 541 VBECLRVGLPREYVNRHCLPCHPCQPONGSVTCFGEADQCVACAHYKDPFPCVARC 600  
 Db 541 VBECLRVGLPREYVNRHCLPCHPCQPONGSVTCFGEADQCVACAHYKDPFPCVARC 600  
 QY 601 PSQVKPDLVMPYIWKFPDEGACQPCINCTHSCVDLDDKGPACORASPLTS----- 653  
 Db 601 PSQVKPDLVMPYIWKFPDEGACQPCINCTHSCVDLDDKGPACORASPLTS----- 653  
 QY 654 ----- 653  
 Db 661 ILLVVVLGVVGLIKERQKIRKTYMRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
 QY 654 ----- 653  
 Db 721 RKVKVLGSGAFGVYKGIWIPDGENVKI PVAIKVLENTSPKANKEILDEAYVMAGVGP 780  
 QY 654 ----- 653  
 Db 781 YVSRLLIGICTSTVQLVQIMPYGLLDHVNRGRGLGSDQLLNWCMAQKMSYLEDVR 840  
 QY 654 ----- 653  
 Db 841 LVHRDLAARNVLKSPNHVKITDFGLRLLDIDETEHADGGKVPKMALESILRRRT 900  
 QY 654 ----- 653  
 Db 901 HQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGBRLPOPPICTTIDVYMIWKWM 960  
 QY 654 -----QNEDLGPASPLDSTFYBSLLEDDMDGLVDA 684  
 Db 961 IDSECRPRFRELVSFMRARDPQRFVITQNEDLGPASPLDSTFYBSLLEDDMDGLVDA 1020  
 QY 685 EYLVLPQQGFPCDPAPGAGMVHRRHR 712  
 Db 1021 EYLVLPQQGFPCDPAPGAGMVHRRHR 1048

RESULT 9  
 ID AAY84780  
 AC AAY84780 standard; Protein; 1255 AA.  
 DT AAY84780;  
 XX  
 XX  
 XX 08-AUG-2000 (first entry)  
 DE Amino acid sequence of the SPLICE erbB-2 receptor protein.  
 XX SPLICE erbB-2 receptor protein; cell transformation disorder; cancer;  
 KW tumor cell proliferation; tissue degeneration; arthropathy;  
 KW bone resorption; inflammatory disease; degenerative disorder;  
 KW wound healing.

XX Homo sapiens.  
 OS WO200020579-A1.  
 PN 13-APR-2000.  
 PD 01-OCT-1999; 99WO-CA00912.  
 PF 02-OCT-1998; 98US-0165192.  
 PR (UWMC-) UNIV MCMASTER.  
 PA Muller WJ, Siegel PM;  
 PI MPI: 2000-303768/26.  
 DR N-PSDB; AAA14812.  
 XX Nucleic acid encoding an erbB 2 receptor protein designated SPLICE  
 PT erbB-2, inhibitors of the protein are useful for treatment of cancer -  
 PS Claim 3; Fig 2; 60pp; English.  
 XX The present sequence represents a SPLICE erbB-2 receptor protein. The  
 CC protein has an in-frame deletion of 16 amino acids, 2 of which are  
 CC conserved cysteine residues, compared to the unspliced protein. The  
 CC erbB-2 polynucleotide is used to construct probes for detecting  
 CC disorders of cell transformation such as cancer. Antibodies to the  
 CC protein may be used to detect SPLICE erbB-2 in a sample. Agents  
 CC (e.g. antisense oligonucleotides) which inhibit the expression of  
 CC SPLICE erbB-2 are useful for reducing tumor cell proliferation and  
 CC treating cancer. Substances which stimulate SPLICE erbB-2 are useful  
 CC for treating conditions of tissue degeneration, such as arthropathy, bone  
 CC resorption, inflammatory diseases, degenerative disorders of the  
 CC central nervous system and wound healing.

XX Sequence 1255 AA;  
 Query Match 95.5%; Score 3776; DB 21; Length 1255;  
 Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
 Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
 QY 1 MELAAALCRWGLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQGCQVQGNL 60  
 Db 1 MELAAALCRWGLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQGCQVQGNL 60  
 QY 61 ELTYLPTNASLSFLQDIQEVQYVLIHNRQVPLQRLRIVRGTLFEDNYALAVLDNG 120  
 Db 61 ELTYLPTNASLSFLQDIQEVQYVLIHNRQVPLQRLRIVRGTLFEDNYALAVLDNG 120  
 QY 121 DPLNNTTPTVGASPGRLRELQRLSITELKGGVLIQRPOLCYQDTILWKDIFHKNQLA 180  
 Db 121 DPLNNTTPTVGASPGRLRELQRLSITELKGGVLIQRPOLCYQDTILWKDIFHKNQLA 180  
 QY 181 LTLIDTNRSRACHPCSPMCKGSRGSESSDCQSLTRTVACGACRCKGPLPTDCCHEQC 240  
 Db 181 LTLIDTNRSRACHPCSPMCKGSRGSESSDCQSLTRTVACGACRCKGPLPTDCCHEQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 QY 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFFETLEETGYLYISAWPDSL 420  
 Db 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFFETLEETGYLYISAWPDSL 420  
 QY 421 DLSVFONLQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNNHLCFVHTV 480



```
Db 421 DLSVFQNLQVIRGRILHNGAYSLSLTQGLGISWLGRLSRLSRLSGGLALIHHTLHLCFVHTV 480
QY 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHQLCARGHCWGPPTQCVCNSQFRLRGQEC 540
Db 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHQLCARGHCWGPPTQCVCNSQFRLRGQEC 540
QY 541 VEECRVLQGLPREYNARHCLPCHPECPQNGSVTCFGEADQCACAHYKDPPEFCVARC 600
Db 541 VEECRVLQGLPREYNARHCLPCHPECPQNGSVTCFGEADQCACAHYKDPPEFCVARC 600
QY 601 PSGVKPDLISYMPIMKFPDEEGACQPCINCTHSCVDLDDKGPABORASPLTS ----- 653
Db 601 PSGVKPDLISYMPIMKFPDEEGACQPCINCTHSCVDLDDKGPABORASPLTSIISAVVG 660
QY 654 ----- 653
Db 661 ILLVVVLGVVFGILIKRRQKIRKYTMRELLQETELVEPLTPSGAMPNQAQMRILKETEL 720
QY 654 ----- 653
Db 721 RKVKVLGSAFCTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDYATVMAGVGP 780
QY 654 ----- 653
Db 781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHRVNRNRLGSLQDLLNMQIAKMSYLEVDVR 840
QY 654 ----- 653
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKGVPKMWALLESILRRFT 900
QY 654 ----- 653
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGPAREIPDLLEKGERLPQPPICTIDVYIMVVKCW 960
QY 654 ----- 653
Db 961 IDSECRPRELVSEFSRWARDPQRFVITQNEIDGLPASPDLSTFYRSLLDDDDMDGLVDA 1020
QY 685 EBYLVPQGGFFCDPAPGAGGMVHRHR 712
Db 1021 EBYLVPQGGFFCDPAPGAGGMVHRHR 1048

RESULT 10
ID AAY92620
XX AAY92620 standard; Protein; 1255 AA.
AC AAY92620;
XX
XX 10-AUG-2000 (first entry)
XX
DE Human heregulin 2 (Her2).
XX
KW Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity;
KW self-protein; cancer; breast cancer; prostate cancer;
KW cell-associated peptide antigen; foreign epitope.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..173
FT /label= N-terminal
FT /note= "mature polypeptide"
FT Region 5..25
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 59..73
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 103..117
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 149..163
```

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FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 174..323
FT /label= Cysteine_rich_domain
FT Region 210..224
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 250..264
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 324..483
FT /label= Ligand_binding_domain
FT Region 325..339
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 369..383
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 465..479
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 484..623
FT /label= Cysteine_rich_domain
FT Region 579..593
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 624..654
FT /label= Transmembrane_domain
FT Region 632..652
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 653..667
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 655..1010
FT /label= Tyrosine_kinase_domain
FT Region 661..675
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 695..709
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 710..730
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 1011..1235
FT /label= C-terminal_domain
```

WO200020027-A2.

13-APR-2000.

05-OCT-1999; 99WO-DK00525.

05-OCT-1998; 98DK-0001261.

20-OCT-1998; 98US-0105011.

(MEBI-) M &amp; E BIOTECH AS.

Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
Gautam A, Birk P, Karlsson G;

WPI; 2000-349917/30.

N-PSDB; AAA09455.

Inducing immune responses to weakly immunogenic, tumor associated  
peptide antigens for the treatment of breast and prostate cancer

Claim 62; Page 193-198; 220pp; English.

This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of  
Her2 can be used in the claimed method as an autovaccine to induce a CTL  
response. Subdominant CTL epitopes, antibody binding regions and

CC cysteine residues involved in disulfide bonds are preserved in the  
CC immunogenized forms. Regions suitable for the insertion of foreign T  
CC helper epitopes were identified (see features table). The method  
CC is used for inducing immune responses against weakly immunogenic  
CC cell-associated peptide antigens (PA) such as those associated with  
CC cancers (self-proteins), e.g. human prostate specific membrane antigen  
CC (PSM), hergulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).  
CC The method comprises effecting simultaneous presentation by antigen  
CC producing cells (APCs) of the animals immune system of: (1) at least 1  
CC CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1  
CC B-cell group derived from the cell-associated PA; and (2) at least 1  
CC first T helper cell group which is foreign to the animal. Analogues of  
CC human PSM, human Her2 and human/murine FGF8b comprising a substantial  
CC part of all known and predicted CTL and B-cell epitopes of the respective  
CC PA and including at least one foreign T helper epitope are also claimed.  
CC The method is used to treat prostate, prostate/breast or breast cancer  
CC when the PA is human PSM, FGF8b and Her2, respectively.  
XX  
SQ Sequence 1255 AA;  
Query Match 95.5%; Score 3776; DB 21; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLIALLPPGAASQVCTGDMKRLRPASPEHLDMLRHLRYQGVVQGNL 60  
DB 1 MELAALCRWGLLIALLPPGAASQVCTGDMKRLRPASPEHLDMLRHLRYQGVVQGNL 60  
QY 61 ELTYLPTNASLSFLDIOEVQGVVLAHNOVQVPLORLRIVRGTOLPEDNYALAVLDNG 120  
DB 61 ELTYLPTNASLSFLDIOEVQGVVLAHNOVQVPLORLRIVRGTOLPEDNYALAVLDNG 120  
QY 121 DPLNNTPTVTGASPGGLRELRLSLTEILKGGVLIQORNPQLCYQDTILWKDIFHKNNQLA 180  
DB 121 DPLNNTPTVTGASPGGLRELRLSLTEILKGGVLIQORNPQLCYQDTILWKDIFHKNNQLA 180  
QY 181 LTLIDTNRGRACHPCSPMKGSRGWESSEDCQSLTRTVAGCARCKGLPTDCHEQC 240  
DB 181 LTLIDTNRGRACHPCSPMKGSRGWESSEDCQSLTRTVAGCARCKGLPTDCHEQC 240  
QY 241 AAGCTGPKHSDCLACHFNHSGTCELHCALVTYNTDFESMNPGRYTFGASCVTACP 300  
DB 241 AAGCTGPKHSDCLACHFNHSGTCELHCALVTYNTDFESMNPGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPHLNQVETAEQGTQCEKSPCARVCYGLGMEHLREVRAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHLNQVETAEQGTQCEKSPCARVCYGLGMEHLREVRAVTSAN 360  
QY 361 IQEFAGCKITFGSLAFIPESFDGDPASNTAPLOPEQLQVFTLEETGYLYISAMPDLSLP 420  
DB 361 IQEFAGCKITFGSLAFIPESFDGDPASNTAPLOPEQLQVFTLEETGYLYISAMPDLSLP 420  
QY 421 DLSVFQNLQVIRGRIHLHNGAYSTIQLGIGTSMGLRSLRELGSGLALIHNTHLCEVHTV 480  
DB 421 DLSVFQNLQVIRGRIHLHNGAYSTIQLGIGTSMGLRSLRELGSGLALIHNTHLCEVHTV 480  
QY 481 PWDLFRNPHOALLHTANRDEDCVCEGLACHQLCARGHCWGPGTQCVCNCSOFLRGQEC 540  
DB 481 PWDLFRNPHOALLHTANRDEDCVCEGLACHQLCARGHCWGPGTQCVCNCSOFLRGQEC 540  
QY 541 VEECRVLQGLPRBYVNAHCLPCHPCQPONGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VEECRVLQGLPRBYVNAHCLPCHPCQPONGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSGVKPDLSPNPTWKPEDEGACQPCPINCTHSCVDLDDKGCFAEORASPLTS----- 653  
DB 601 PSGVKPDLSPNPTWKPEDEGACQPCPINCTHSCVDLDDKGCFAEORASPLTSIVSAVVG 660  
QY 654 ----- 653  
DB 661 ILLVVVLGVVFGILIKRQOKIRKTYMRLLQETELVEPLTPSGAMPNQAMRLKETEL 720  
QY 654 ----- 653

DB 721 RKVKVLGSGARFTVYGIWIPDGENVKIPVAIKVLRENTSPKANKEILLDEAYVMAGVGP 780  
QY 654 ----- 653  
DB 781 YVSRLLGICLTSTVQLVTQMPYGCILLDHVRENRLGSLQDILLNWCMIKAGMSYLEVDR 840  
QY 654 ----- 653  
DB 841 LVHRDLAARNVLKSPNHNKIDTDFGLARLLDIDETEHADGKVPKIKWALESIILRRPT 900  
QY 654 ----- 653  
DB 901 HQSDVWSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICTIDVYIMVWKWM 960  
QY 654 ----- QNEDLGSPASPLDSTFYRSLEDDDDMGDLVDA 684  
DB 961 IDSECRPRFRELVSFERSWARDPQRFVVIQNEEDLGSPASPLDSTFYRSLEDDDDMGDLVDA 1020  
QY 685 BEYLVPQGGFFCPDPAPGAGGMVHRHR 712  
DB 1021 BEYLVPQGGFFCPDPAPGAGGMVHRHR 1048  
RESULT 11  
ID AA012130 standard; Protein; 1255 AA.  
XX AA012130;  
XX 18-DEC-2001 (first entry)  
XX Human tyrosine kinase-type receptor, HER-2.  
XX Therapeutic compound; major histocompatibility complex; vaccine;  
XX antigenic peptide; MHC; immunoregulatory; immune response; HER-2;  
XX adoptive immunotherapy; anti-cancer; breast cancer antigen; APC;  
XX antigen presenting cell; human; tyrosine kinase-type receptor.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 774..782  
FT /note= "Antigenic epitope"  
XX WO200168677-A2.  
XX 20-SEP-2001.  
XX 16-MAR-2001; 2001WO-US40328.  
XX 16-MAR-2000; 2000US-0527487.  
XX (GENZ ) GENZYME CORP.  
XX Nicolette CA;  
XX WPI; 2001-616284/71.  
XX N-PSDB; AAD19731.  
XX Novel synthetic therapeutic compound for inducing immune response and  
XX for use in adoptive immunotherapy, has enhanced binding to major  
XX histocompatibility molecules and enhanced immunoregulatory properties  
XX  
XX Claim 4; Page 63-67; 69pp; English.  
XX The invention relates to synthetic therapeutic compounds (antigenic  
XX peptides) with enhanced binding to major histocompatibility complex  
XX (MHC) molecules and enhanced immunoregulatory properties relative  
XX to their natural counterparts. Compounds of the invention are useful  
XX for inducing an immune response in a subject and for use in adoptive  
XX immunotherapy. They are useful as components of anti-cancer vaccines

CC and to expand immune effector cells that are specific for cancers  
CC characterised by expression of the breast cancer antigen, HER-2.  
CC Polynucleotides that encode peptides of the invention are useful as  
CC hybridisation probes and as primers for the detection of genes of gene  
CC transcripts that are expressed in antigen presenting cells (APCs), to  
CC confirm transduction of polynucleotides into host cells. The present  
CC sequence is human tyrosine kinase-type receptor, HER-2. Compounds  
CC of the invention are designed based on the HER-2 antigenic peptide  
XX (774-782).  
XX  
SQ Sequence 1255 AA;  
Query Match 95.5%; Score 3776; DB 22; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRHLVQCGVQGNL 60  
DB 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRHLVQCGVQGNL 60  
QY 61 ELTYLPTNASLFLQDIQEVQGVLIHNVQVPLQRLRIVRGTQLFEDNYVALVLDNG 120  
DB 61 ELTYLPTNASLFLQDIQEVQGVLIHNVQVPLQRLRIVRGTQLFEDNYVALVLDNG 120  
QY 121 DPLNNTPTVTGASPGGLRELQRLRSLEILKGVLIQRPOLCYQDTILWKDIFHKNOLA 180  
DB 121 DPLNNTPTVTGASPGGLRELQRLRSLEILKGVLIQRPOLCYQDTILWKDIFHKNOLA 180  
QY 181 LTLIDTNSRACHPCSPCKGRCGSESDCOSLTRVCAGGCARCKGPLTDCCHQC 240  
DB 181 LTLIDTNSRACHPCSPCKGRCGSESDCOSLTRVCAGGCARCKGPLTDCCHQC 240  
QY 241 AAGCTGPKHSDCLACILFHNHSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300  
DB 241 AAGCTGPKHSDCLACILFHNHSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVAVTSAN 360  
QY 361 IQEFAGCKIIFGLAFPLSPFGDPAASNTAPLQPEQLQVFETLEITGYLISAWPDSL 420  
DB 361 IQEFAGCKIIFGLAFPLSPFGDPAASNTAPLQPEQLQVFETLEITGYLISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLSLRELGLALHNNHLCFVHTV 480  
DB 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLSLRELGLALHNNHLCFVHTV 480  
QY 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWPGPTQCVNCSQFLRGQEC 540  
DB 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWPGPTQCVNCSQFLRGQEC 540  
QY 541 VZECRVQLPREYNARHCLCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VZECRVQLPREYNARHCLCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSGVXPDLISYMPIWKPFPDEGACQPCINCTHSCVDLDDKGPASORASPLTS 653  
DB 601 PSGVXPDLISYMPIWKPFPDEGACQPCINCTHSCVDLDDKGPASORASPLTS 653  
QY 654 ----- 653  
DB 661 ILLVVVLGVVGLIKRRQKIRKYTMRELLQETELVEPLTPSGAMPNQAQMRILKETEL 720  
QY 654 ----- 653  
DB 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVSP 780  
QY 654 ----- 653  
DB 781 YVSRLLGICLTSTVLQVLMQPYGCLLDHVRNRRGLSGQDILLNMCMIAGMSYLEDR 840  
QY 654 ----- 653

DB 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKIKMALESILRRRT 900  
QY 654 ----- 653  
DB 901 HQSDVWSYGVTVWELMTFGAXPYDGIPIAREIPDLLEKGERLPQPPICTIDVYMINVKCWM 960  
QY 654 -----QNEGLGPASPLDSTFYRSLLDDMDGDLVDA 684  
DB 961 IDSECRPRFRELVSFESRMARDPQRFVVIQNEGLGPASPLDSTFYRSLLDDMDGDLVDA 1020  
QY 685 BEYLVPQGFPCPDPAAGAGGMVHRHR 712  
DB 1021 BEYLVPQGFPCPDPAAGAGGMVHRHR 1048  
RESULT 12  
AAB85458 standard; Protein; 1255 AA.  
XX  
AC AAB85458;  
DT 25-SEP-2001 (first entry)  
XX  
DE Human HER-2/neu protein.  
XX  
KW Antigen-presenting cell; immunogenic; immune response; HER-2/neu;  
XX oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.  
XX  
OS Homo sapiens.  
XX  
PN WO200153463-A2.  
PD 26-JUL-2001.  
XX  
PF 19-JAN-2001; 2001WO-US01850.  
PR 21-JAN-2000; 2000US-0177545.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Cheever MA, Hand-Zimmermann S;  
XX  
DR WPI; 2001-476112/51.  
XX  
DR N-PSDB; AAH23392.  
XX  
PT New antigen-presenting cells, useful as vaccines for eliciting or  
PT enhancing an immune response to HER-2/neu protein, particularly useful  
PS for treating or preventing cancer, e.g. breast cancer -  
PS Claim 2; Page 41-46; 49pp; English.  
XX  
CC The invention provides an isolated antigen-presenting cell, which  
CC expresses at least an immunogenic portion of a polypeptide that produces  
CC an immune response to HER-2/neu protein. The antigen-presenting cells are  
CC useful as vaccines for eliciting or enhancing an immune response to  
CC HER-2/neu protein, particularly in treating or preventing malignancies in  
CC which the HER-2/neu oncogene is associated. Specifically, these are  
CC useful for treating or preventing cancer, e.g. breast cancer, ovarian,  
CC colon, lung or prostate cancers. The present sequence represents  
CC the human HER-2/neu protein (also known as p185 or c-erbB2).  
XX  
SQ Sequence 1255 AA;  
Query Match 95.5%; Score 3776; DB 22; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRHLVQCGVQGNL 60  
DB 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRHLVQCGVQGNL 60  
QY 61 ELTYLPTNASLFLQDIQEVQGVLIHNVQVPLQRLRIVRGTQLFEDNYVALVLDNG 120

Db 61 ELTYLPTNASLSFLQDIOEVQGVLIHAHQVRQVPLQRLRIVRGTFQFEDNYALAVLDNG 120  
QY 121 DPLNNTTPVTGASPGGLRELQRLSLTEILKGGVLIQIORNPOLCYQDTILWKDIFHKNNQLA 180  
Db 121 DPLNNTTPVTGASPGGLRELQRLSLTEILKGGVLIQIORNPOLCYQDTILWKDIFHKNNQLA 180  
QY 181 LTLIDNRSRACHPCSPMCKGSRGSGESSEDQSLTRTVTCAGCARCKGPLPTDCCHEQC 240  
Db 181 LTLIDNRSRACHPCSPMCKGSRGSGESSEDQSLTRTVTCAGCARCKGPLPTDCCHEQC 240  
QY 241 AAGCTGPKSDCLACLHFNHSGICELHCPALVTYNTDTPESMPNBPGRYTFGASCVTACP 300  
Db 241 AAGCTGPKSDCLACLHFNHSGICELHCPALVTYNTDTPESMPNBPGRYTFGASCVTACP 300  
QY 301 YNYLSTVDSCTLVCPHNOEVTAEQGTORCEKSKPCARVCVGLGMEHLREVRVTSAN 360  
Db 301 YNYLSTVDSCTLVCPHNOEVTAEQGTORCEKSKPCARVCVGLGMEHLREVRVTSAN 360  
QY 361 IQEFAGCKIFGSLAFPLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLISAMPDSL 420  
Db 361 IQEFAGCKIFGSLAFPLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLISAMPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGSIWGLSLRELSGGLALIHNNTHLCFVHTV 480  
Db 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGSIWGLSLRELSGGLALIHNNTHLCFVHTV 480  
QY 481 PDQLFRNPHQALHTANRPEDESCVGEGLACHQLCARGHCWGPGTQCVCNCSQFLRGQBC 540  
Db 481 PDQLFRNPHQALHTANRPEDESCVGEGLACHQLCARGHCWGPGTQCVCNCSQFLRGQBC 540  
QY 541 VECRLVQLPREYVNAHCLPCHPCQPNQSGSVTCFGEADQCVACAHYKDPFPFCVARC 600  
Db 541 VECRLVQLPREYVNAHCLPCHPCQPNQSGSVTCFGEADQCVACAHYKDPFPFCVARC 600  
QY 601 PSQVKPDLSPYIWKFPDEBAGACQPCINCTHSCVDLDDKGCAPORASPLTS----- 653  
Db 601 PSQVKPDLSPYIWKFPDEBAGACQPCINCTHSCVDLDDKGCAPORASPLTS----- 653  
QY 654 ----- 653  
Db 661 ILLVWLVGVVGLIKRQOKIRKYTMRLLOETELVEPLTPSGAMPNQAQMRILKETEL 720  
QY 654 ----- 653  
Db 721 RKVVLGSGAFGVYKGIWIPDGENVKIPVAIKVLRNTSPKANKILDEAYVMAGVGSF 780  
QY 654 ----- 653  
Db 781 YVSRLLGICLTSTVQLVTLQMPYGCLLDHVRENRLGRLGSDLLNWCQIAKGMVYLEDVR 840  
QY 654 ----- 653  
Db 841 LVHRDLAARNVLKSPNHVKITDGLARLLIDETEHADGGKVPKWMALBSILRRRT 900  
QY 654 ----- 653  
Db 901 HQSDVWSYGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPICTIDVYMWKCM 960  
QY 654 -----QNEDLGPASPLDSTFYRSLLLEDMDGLDVA 684  
Db 961 IDSECRPRFRELVSFSESRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLLEDMDGLDVA 1020  
QY 685 EYLVPOQGFCDPAPAGGMVHHRH 712  
Db 1021 EYLVPOQGFCDPAPAGGMVHHRH 1048

RESULT 13  
AAG88267  
ID AAG88267 standard; Protein; 1255 AA.  
XX  
AC AAG88267;

XX 11-SEP-2001 (first entry)  
XX HER2/neu amino acid sequence.  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; cancer; cytotoxic; immunostimulant;  
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX Homo sapiens.  
XX WO200141787-A1.  
XX 14-JUN-2001.  
XX 11-DEC-2000; 2000WO-US33591.  
XX 10-DEC-1999; 99US-0458299.  
XX (EPIM-) EPIMMUNE INC.  
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX Keogh E;  
XX WPI; 2001-374995/39.  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer -  
XX Disclosure; Page 15; 1999p; English.  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX As described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising  
XX (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic  
XX and immunostimulant activities, and can be used in vaccines. (I), (II)  
XX and (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention.  
XX Sequence 1255 AA;  
XX Query Match 95.5%; Score 3776; DB 22; Length 1255;  
XX Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
XX Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELALCRWGLLALLPGCAASTQVCTGDMKRLPASPETHLDMRLHLYQCQVQGNL 60  
Db 1 MELALCRWGLLALLPGCAASTQVCTGDMKRLPASPETHLDMRLHLYQCQVQGNL 60  
QY 61 ELTYLPTNASLSFLQDIOEVQGVLIHAHQVRQVPLQRLRIVRGTFQFEDNYALAVLDNG 120  
Db 61 ELTYLPTNASLSFLQDIOEVQGVLIHAHQVRQVPLQRLRIVRGTFQFEDNYALAVLDNG 120  
QY 121 DPLNNTTPVTGASPGGLRELQRLSLTEILKGGVLIQIORNPOLCYQDTILWKDIFHKNNQLA 180

```
Db 121 DPLNNTPTVTGASPGRLRELQRLSLTEILKGGVLIQRNPOLCYQDTILWKDIFHKNNQLA 180
QY 181 LTLIDTNRSRACHPCSPMKGSRGWESSEDCOSLTRTVTCAGGCARCKGPLPTDCCHQC 240
Db 181 LTLIDTNRSRACHPCSPMKGSRGWESSEDCOSLTRTVTCAGGCARCKGPLPTDCCHQC 240
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
QY 301 YNYLSTDVGSCTLVCPHLNQVTAEDGTORCEKSKPCARVCYGLGMHLEHREVAVTSAN 360
Db 301 YNYLSTDVGSCTLVCPHLNQVTAEDGTORCEKSKPCARVCYGLGMHLEHREVAVTSAN 360
QY 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEETGYLYISAWPDSL 420
Db 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEETGYLYISAWPDSL 420
QY 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480
Db 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480
QY 481 PNDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPGTQCVCNCSQFLRGQC 540
Db 481 PNDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPGTQCVCNCSQFLRGQC 540
QY 541 VBECRVLQGLPREYVNAHCLPCHPCQPNQSGVTCFGEADQCVACAHYKDPFPCVAPC 600
Db 541 VBECRVLQGLPREYVNAHCLPCHPCQPNQSGVTCFGEADQCVACAHYKDPFPCVAPC 600
QY 601 PSQVPEDLSPYPIKFPDEEGACQPCPNCTHSCVDLDDKGCFAQASPLTS----- 653
Db 601 PSQVPEDLSPYPIKFPDEEGACQPCPNCTHSCVDLDDKGCFAQASPLTSIIISAVVG 660
QY 654 ----- 653
Db 661 ILLVVVLGVVFGILIKRQOKIRKVTMRRLQETELVEPLTPSGAMPNQAOMRILKETEL 720
QY 654 ----- 653
Db 721 RKVKVLGSGAFGVYKGIWIPDGENVKIIPVALKVLRENTSPKANKEILDEATVMAGVSP 780
QY 654 ----- 653
Db 781 YVSRLLGICLTSTVQLVTQMLPYGCLLDHVRNRLGSLQDLNNWCMIKAGWSYLEDVR 840
QY 654 ----- 653
Db 841 LVHRLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMALLESILRRRPT 900
QY 654 ----- 653
Db 901 HQSDVWSVGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPICTIDVYIMVWKCM 960
QY 654 -----QNEDLGPASPLDSTFYRSLLLEDDMDGLDVA 684
Db 961 IDSECRPRELVSFERSWARDPQRFVVIQNEDLGPASPLDSTFYRSLLLEDDMDGLDVA 1020
QY 685 BEYLVPOQGFPCDPAPGAGMVHRRH 712
Db 1021 BEYLVPOQGFPCDPAPGAGMVHRRH 1048
```

## RESULT 14

AAB60167

ID AAB60167 standard; Protein; 1255 AA.

XX

AC AAB60167;

XX

DT 03-APR-2001 (first entry)

XX

DE HER2 transgene plasmid construct encoded protein.

```
XX Human; HER2; ErbB2 receptor; p185neu; maytansinoid conjugate; cancer;
KW antibody.
XX Homo sapiens.
OS Synthetic.
XX WO200100244-A2.
XX PD 04-JAN-2001.
XX 23-JUN-2000; 2000WO-US17229.
XX 25-JUN-1999; 99US-0141316.
PR 16-MAR-2000; 2000US-0189844.
PA (GETH ) GENENTECH INC.
XX Erickson S, Schwall R;
XX WPI; 2001-061962/07.
DR N-PSDB; AAF24297.
XX Treating tumors, particularly breast cancers, which overexpress an ErbB
PT receptor and does not respond to an anti-ErbB antibody, comprises
PT conjugating the antibody to a maytansinoid -
XX Example 3; Fig 4; 92pp; English.
XX The present invention provides a method of treating cancer by
CC administering a conjugate of anti-ErbB antibody with a maytansinoid. In
CC particular, the antibody is directed against ErbB2 (also known as HER2
CC and p185neu). The method is particularly useful in the treatment of
CC breast, ovarian, stomach, endometrial, salivary gland, lung, kidney,
CC colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
XX SQ Sequence 1255 AA;
```

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Query Match 95.5%; Score 3776; DB 22; Length 1255;
Best Local Similarity 67.9%; Pred. No. 6, 6e-285;
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;
QY 1 MELAALCRWGLLLALLPPGAASVQCTCTDMKRLPASPETHLDMRLHYQCQVQGNL 60
Db 1 MELAALCRWGLLLALLPPGAASVQCTCTDMKRLPASPETHLDMRLHYQCQVQGNL 60
QY 61 ELTYLPTNASLSPLODIOEVQGVLIHNVQVPLQRLRIVRGTLQEDNYALAVLNG 120
Db 61 ELTYLPTNASLSPLODIOEVQGVLIHNVQVPLQRLRIVRGTLQEDNYALAVLNG 120
QY 121 DPLNNTPTVTGASPGRLRELQRLSLTEILKGGVLIQRNPOLCYQDTILWKDIFHKNNOLA 180
Db 121 DPLNNTPTVTGASPGRLRELQRLSLTEILKGGVLIQRNPOLCYQDTILWKDIFHKNNOLA 180
QY 181 LTLIDTNRSRACHPCSPMKGSRGWESSEDCOSLTRTVTCAGGCARCKGPLPTDCCHQC 240
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Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
QY 301 YNYLSTDVGSCTLVCPHLNQVTAEDGTORCEKSKPCARVCYGLGMHLEHREVAVTSAN 360
Db 301 YNYLSTDVGSCTLVCPHLNQVTAEDGTORCEKSKPCARVCYGLGMHLEHREVAVTSAN 360
QY 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEETGYLYISAWPDSL 420
Db 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEETGYLYISAWPDSL 420
QY 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480
Db 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480
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QY 481 PWDQFRNPHOALLHTANRPEDEVCVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
DB 481 PWDQFRNPHOALLHTANRPEDEVCVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSVKPDLSPYMPKPPDEGACQPCPINCTHSCVDLDDKGCPCAEQASPLTS----- 653  
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QY 654 ----- 653  
DB 661 ILLVVVLGVVFGILIKRQOKIRKYMRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
QY 654 ----- 653  
DB 721 RKVVLGSGAGFTYKGIWIPDGENVKIPVAIKVLRNTPKANKELDEAYVMAGVGSF 780  
QY 654 ----- 653  
DB 781 YVSRLLGICLTSTVQLVTLQMPYGCCLLDHVRENRLGSLQDILLNWCWQIAKGMXYLEDVR 840  
QY 654 ----- 653  
DB 841 LVHRDLAARNVLVKSNNHVKITDFGLARLLDIDETEHADGGKVPKVMMALESILRRRT 900  
QY 654 ----- 653  
DB 901 HQSDVMSYGVTVWELMTFGAKPYDIPAREIPDLEKGERLPQPPICITDVYIMVYKWM 960  
QY 654 -----ONEDLGASPLDSTFYRSLLDDDDMGDLVDA 684  
DB 961 IDSECRPRRELVSFERSMARDPQRFVIONEDLGASPLDSTFYRSLLDDDDMGDLVDA 1020  
QY 685 EYLVPOQGFCDPAPGAGMVRHR 712  
DB 1021 EYLVPOQGFCDPAPGAGMVRHR 1048

RESULT 15  
AAE26349  
ID AAE26349 standard; Protein; 1255 AA.  
XX AC AAE26349;  
DT 13-DEC-2002 (first entry)  
DE Human HER-2 protein.  
XX Transgenic animal; transgenic; mammary gland cell; HER2; tumour;  
KW cancer; therapy; apoptosis; cytostatic; human.  
XX Homo sapiens.  
XX US2002035736-A1.  
XX 21-MAR-2002.  
XX 16-MAR-2001; 2001US-0811115.  
XX 16-MAR-2000; 2000US-189844P.  
XX (ERIC/) ERICKSON S.  
PA (KING/) KING K.  
PA (SCHW/) SCHWALL R.  
XX Erickson S, King K, Schwall R;  
PI WPI; 2002-401155/43.  
DR N-PSDB; AAD43934, AAD43935.

XX New transgenic non-human mammal that produces detectable levels of a  
PT native human HER2 protein in its mammary gland cells, useful as tumor  
PT models for testing HER2-directed cancer therapies, and for identifying  
PT anticancer agents  
XX Example 2; Page 26-29; 83pp; English.  
XX The invention relates to a transgenic non-human mammal that produces in  
CC its mammary gland cells detectable levels of a native human HER2 protein  
CC or its fragment. The transgenic animals are useful as tumor models for  
CC testing HER2-directed cancer therapies, and for identifying anticancer  
CC agents. The animals may also be used as source of cells which can be  
CC immortalised in culture, in screening for compounds that have potential  
CC as prophylactic or therapeutic treatments for diseases or disorders  
CC involving expression of HER2. The anti-cancer molecules are useful for  
CC inducing apoptosis or cell death of cancer cells. The present sequence  
CC is human HER-2 protein.  
XX Sequence 1255 AA;  
QY Query Match 95.5%; Score 3776; DB 23; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQCGVQGNL 60  
DB 1 MELAALCRWGLLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQCGVQGNL 60  
QY 61 ELYLPTNASLFLQDIQEVQGVLIANQVRQVFLRLRIVRGTLQFEDNVALAVLNG 120  
DB 61 ELYLPTNASLFLQDIQEVQGVLIANQVRQVFLRLRIVRGTLQFEDNVALAVLNG 120  
QY 121 DPLNNTPTVGTASPGRLRELQRLSITELKGVLTORNPOLCVQDTILWKDIFHKNQLA 180  
DB 121 DPLNNTPTVGTASPGRLRELQRLSITELKGVLTORNPOLCVQDTILWKDIFHKNQLA 180  
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DB 181 LTLIDTNRSRACHPCSPCKSGRCSESDQCSLRTVTCAGGCARCKGPLPTDCCHEQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCFALVTYNTDTPESMPNPEGRYTFGASCVTAC 300  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCFALVTYNTDTPESMPNPEGRYTFGASCVTAC 300  
QY 301 YNYLSTDVGSCTLVCPHNOEVTAEQTCRCKSKPCARVCYGLGMEHLREVAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHNOEVTAEQTCRCKSKPCARVCYGLGMEHLREVAVTSAN 360  
QY 361 IOEFAGCKKIFGSLAFPLPESFDGDPASNTAPLQPELOQVFTLEETGLYISAWPDSL 420  
DB 361 IOEFAGCKKIFGSLAFPLPESFDGDPASNTAPLQPELOQVFTLEETGLYISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSLTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
DB 421 DLSVFQNLQVIRGRILHNGAYSLTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
QY 481 PWDQLFRNPHOALLHTANRPEDEVCVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
DB 481 PWDQLFRNPHOALLHTANRPEDEVCVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSVKPDLSPYMPKPPDEGACQPCPINCTHSCVDLDDKGCPCAEQASPLTS----- 653  
DB 601 PSVKPDLSPYMPKPPDEGACQPCPINCTHSCVDLDDKGCPCAEQASPLTSIVSAVVG 660  
QY 654 ----- 653  
DB 661 ILLVVVLGVVFGILIKRQOKIRKYMRLLQETELVEPLTPSGAMPNQAMRILKETEL 720

Qy 654 ----- 653  
Db 721 RKVKVLGSGAGCTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGP 780  
Qy 654 ----- 653  
Db 781 YVSRLLGICLTSTVQLVTQMPYGCLLDHVRENRRGLSGODLLNWCMIKMGMSYLEDVR 840  
Qy 654 ----- 653  
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHYHADGGKVPKMWALESIILRRFT 900  
Qy 654 ----- 653  
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPPICTIDVYIMVVKCWM 960  
Qy 654 ----- QNEDLGASPLDSTFYRSLLDDDDMGDLVDA 684  
Db 961 IDSECRPRFRELVSFERNARDPQRFVVTQNEEDLGASPLDSTFYRSLLDDDDMGDLVDA 1020  
Qy 685 EYLVPPQGGFFCPCDPAGAGGMVHHR 712  
Db 1021 EYLVPPQGGFFCPCDPAGAGGMVHHR 1048

Search completed: December 5, 2003, 14:33:25  
Job time : 46.3599 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 5, 2003, 14:26:38 ; Search time 45.6401 Seconds  
(without alignments)  
3196.087 Million cell updates/sec

Title: US-09-854-356-6

Perfect score: 5078

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5078	100.0	919	21	Human Her-2/neu fu
2	5078	100.0	919	23	Her-2/neu extracel
3	4900	96.5	1255	17	Human HER-2/neu protein.
4	4900	96.5	1255	20	Human HER-2/neu on
5	4900	96.5	1255	21	Human HER-2/neu pr
6	4900	96.5	1255	21	Amino acid sequenc
7	4900	96.5	1255	22	Human HER-2/neu pr
8	4900	96.5	1255	22	HER2/neu amino aci
9	4900	96.5	1255	23	Human Her-2 protei

10	4900	96.5	1255	23	AAE20479	Human Her-2/neu pr
11	4900	96.5	1255	23	AAAM51143	Human Her-2/neu po
12	4900	96.5	1255	23	AAU77114	Human heregulin 2
13	4892	96.3	1255	21	AAAY92620	Human tyrosine kin
14	4892	96.3	1255	22	AAE12130	HER2 transgene pla
15	4892	96.3	1255	22	AAAG60167	Human HER-2 protei
16	4892	96.3	1255	23	AAE26349	Human HER2 antige
17	4892	96.3	1255	23	AAE26366	Human HER2 (ErBB2)
18	4892	96.3	1255	23	AAU74545	Breast cancer asso
19	4892	96.3	1255	24	ABR47447	Human Her-2/neu pro
20	4892	96.3	1255	24	ABP74708	Sequence of c-erbB
21	4857	95.6	1433	14	AAK39568	Human breast cance
22	4722	93.0	1223	23	AAU98923	Human HER-2/neu ex
23	4583	90.3	1200	21	AAAB21208	Mouse Her-2/neu ex
24	4309.5	84.9	920	23	AAAM51152	Mouse Her-2/neu ex
25	4309.5	84.9	926	23	AAAM51153	Rat Her-2/neu prot
26	4138.5	81.5	1256	21	AAAB21199	Rat Her-2/neu onco
27	4138.5	81.5	1256	23	AAAM51144	Mouse Her-2/neu pr
28	4125.5	81.2	1256	21	AAAB21206	Amino acid sequenc
29	4125.5	81.2	1256	22	AAAG2860	Mouse Her-2/neu on
30	4125.5	81.2	1256	23	AAAM51151	Human HER-2/neu fu
31	3954	77.9	712	23	AAAB21204	Her-2/neu extracel
32	3954	77.9	712	23	AAAM51149	Her-2-GM-CSF immuno
33	3632	71.5	782	18	AAW19764	Extracellular HER-
34	3628	71.4	653	21	AAAB21200	Human Her-2/neu on
35	3628	71.4	653	23	AAAM51145	Human ErbB2 oncopr
36	3590	70.7	645	22	AAAB60408	Human ErbB2 extrac
37	3590	70.7	645	23	AAAB61593	Human HER2 recepto
38	3590	70.7	645	23	ABG70753	DC8scFv-erbB2EC fu
39	3525	69.4	951	21	AAAY44993	Extracellular port
40	3422	67.4	624	11	AAAR08222	Rat Her-2/neu prot
41	3110.5	61.3	654	21	AAAB21205	Rat Her-2/neu onco
42	3110.5	61.3	654	23	AAAM51150	Human HER500 fusio
43	2585	50.9	564	22	AAE13110	Human HER500-rGM-C
44	2585	50.9	564	22	AAE13111	Human HER500 fusio
45	2573.5	50.7	555	22	AAE13108	

#### ALIGNMENTS

```

RESULT 1
AAAB21203
ID AAB21203 standard; protein; 919 AA.
XX
AC AAB21203;
XX
DT 12-JAN-2001 (first entry)
XX
DE Human HER-2/neu fusion protein.
XX
KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW colon cancer; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044899-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02164.
XX
PR 29-JAN-1999; 99US-0117976.
XX
(CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM.
XX
PI Cheever MA, Gheysen D;
XX
WPI; 2000-505976/45.
XX

```

PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
PT useful for vaccinating against breast, ovarian, colon, lung and  
PS prostate cancers -  
XX Claim 2; Fig 12; 128pp; English.

CC The present sequence is a fusion protein comprising the extracellular  
CC domain and the phosphorylation domain of the human HER-2/neu protein.  
CC HER-2/neu is a member of the tyrosine kinase family of receptor-like  
CC glycoproteins and shows homology to the epidermal growth factor receptor  
CC (EGFR). It probably plays a part in cell growth and/or differentiation.  
CC The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used  
CC to treat or prevent cancer by eliciting or enhancing an immune response  
CC to the HER-2/neu protein. They may be used to treat malignancies such as  
CC breast, ovarian, colon, lung and prostate cancers, and may be used as an  
CC antigen to vaccinate against these neoplasias.

XX SQ Sequence 919 AA;  
Query Match 100.0%; Score 5078; DB 21; Length 919;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMLRHLVQGCQVQGNL 60  
Db 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMLRHLVQGCQVQGNL 60  
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Db 61 ELTYLPTNASLSFLQDIOEQVGVLAHNOVQVPLRIVRGTOLPEDNALAVLDNG 120  
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Db 121 DPLNNTPTVGTASPGGLRELRLSLTEILKGGVLIQNPQLCYQDFTLWKDIFHKNNOLA 180  
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QY 541 VEECRVLQGLPREYVNRHCLPCHPECQPNQSGSVTCFGEADQCVACAHYKPPFCVARC 600  
Db 541 VEECRVLQGLPREYVNRHCLPCHPECQPNQSGSVTCFGEADQCVACAHYKPPFCVARC 600  
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Db 901 FKGTPTAENPEYLGLDVVP 919

RESULT 2  
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ID AAM51148 standard; Protein; 919 AA.  
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AC AAM51148;  
DT 17-JUN-2002 (first entry)  
XX  
DE Her-2/neu extracellular domain-phosphorylation domain fusion.  
KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 1..653  
FT /note= "extracellular domain"  
FT Domain 654..919  
FT /note= "phosphorylation domain"  
XX WO200212341-A2  
XX 14-FEB-2002.  
XX  
XX 03-AUG-2001; 2001WO-US24283.  
XX 03-AUG-2000; 2000US-0632507.  
XX (CORI-) CORIXA CORP.  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Cheever MA, Gheysen D;  
XX WPI; 2002-241743/29.  
XX  
XX Her-2/neu fusion protein for treating or preventing cancer by eliciting  
XX or enhancing an immune response to the protein, has Her-2/neu  
XX extracellular domain fused to Her-2/neu intracellular or  
XX phosphorylation domain  
XX Claim 2; Fig 12; 141pp; English.  
XX  
XX The present sequence is that of a fusion protein between the  
XX extracellular domain and phosphorylation domain of human Her-2/neu  
XX (see AAM51143), an oncogenic self-protein and target for anti-cancer  
XX vaccines. The fusion protein can be obtained by recombinant DNA  
XX methods. Her-2/neu overexpression correlates with a poor prognosis  
XX in breast and ovarian cancers. The invention provides Her-2/neu  
XX fusion proteins, nucleic acids encoding them, viral vectors, and  
XX vaccines comprising the fusion proteins or nucleic acid molecules.  
XX In preferred fusion proteins, the extracellular domain of a  
XX Her-2/neu protein is fused to a Her-2/neu intracellular domain or  
XX phosphorylation domain (or its DeltaPD fragment). An immune  
XX response to Her-2/neu protein is elicited or enhanced by  
XX administering the fusion protein in the form of a vaccine, or by  
XX transfecting cells of an animal ex vivo with a nucleic acid  
XX encoding the fusion protein, and delivering the transfected cells

CC to the animal. The fusion proteins, nucleic acids, and isolated  
 CC specific T-cells are useful for inhibiting the development of a  
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer  
 CC in a patient. T cells that specifically react with a Her-2/neu  
 CC fusion protein can be used to remove tumour cells from a sample in  
 CC order to inhibit the development of cancer in a patient.  
 XX  
 SQ Sequence 919 AA;  
 Query Match 100.0%; Score 5078; DB 23; Length 919;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MELALCRWGLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHLYQCQVQGNL 60  
 DB 1 MELALCRWGLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHLYQCQVQGNL 60  
 QY 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIRVGTQLPEDNVALAVLNG 120  
 DB 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIRVGTQLPEDNVALAVLNG 120  
 QY 121 DFLNNTTPTVGASPGCLRELQRLSLEILKGGVLIQRPOLCVQDTILWKDIFHKNQOLA 180  
 DB 121 DFLNNTTPTVGASPGCLRELQRLSLEILKGGVLIQRPOLCVQDTILWKDIFHKNQOLA 180  
 QY 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRTVACGCCARCKGPLEPTDCHEQC 240  
 DB 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRTVACGCCARCKGPLEPTDCHEQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300  
 DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNLSLTDVSGCTLVCPHNOVTADGTQRCCKPCARVCYGLGMEHLREVRAVTSAN 360  
 DB 301 YNLSLTDVSGCTLVCPHNOVTADGTQRCCKPCARVCYGLGMEHLREVRAVTSAN 360  
 QY 361 IQEFAGCKKIFGSLAFPLPSFGDPSANTAPQLQVFELEITGYLISAWPDSLP 420  
 DB 361 IQEFAGCKKIFGSLAFPLPSFGDPSANTAPQLQVFELEITGYLISAWPDSLP 420  
 QY 421 DLSVFQNLQVIRILHNGAYSILTLQGLIGSLWGLRLSRLSGLALIHNTLHCFVHTV 480  
 DB 421 DLSVFQNLQVIRILHNGAYSILTLQGLIGSLWGLRLSRLSGLALIHNTLHCFVHTV 480  
 QY 481 PWDQLFRNPHQALLHTANRPEDECYEGGLACHQLCARGHCWGPPTQVCNCSQFLRGQEC 540  
 DB 481 PWDQLFRNPHQALLHTANRPEDECYEGGLACHQLCARGHCWGPPTQVCNCSQFLRGQEC 540  
 QY 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
 DB 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
 QY 601 PSQVFPDLSYMPIKFPDDEGACQPCINCTHSCVDLDDKGPAPQASPLTSQNEIDLGP 660  
 DB 601 PSQVFPDLSYMPIKFPDDEGACQPCINCTHSCVDLDDKGPAPQASPLTSQNEIDLGP 660  
 QY 661 ASPLDSTFVRSLELDDMDGLVDAEYLVPQGFPCPDPAAGGVMVHRHSSSTRSGG 720  
 DB 661 ASPLDSTFVRSLELDDMDGLVDAEYLVPQGFPCPDPAAGGVMVHRHSSSTRSGG 720  
 QY 721 GDLTLGLEPSEEPAPSLAPSEGAGSDVFDGLGMAAKGLQSLPDPSPLOQVSEDP 780  
 DB 721 GDLTLGLEPSEEPAPSLAPSEGAGSDVFDGLGMAAKGLQSLPDPSPLOQVSEDP 780  
 QY 781 TVPLRSETDGYVAPLTCSQPPYVNPQVVRPQPPSPREGPLPAAPAGATLSPKTLSPG 840  
 DB 781 TVPLRSETDGYVAPLTCSQPPYVNPQVVRPQPPSPREGPLPAAPAGATLSPKTLSPG 840  
 QY 841 KNGVVKDVPFAGGAVENPBYLTQGGAAAPQHPHPPAFSPAFNLVYWDQDPPERGAPPST 900  
 DB 841 KNGVVKDVPFAGGAVENPBYLTQGGAAAPQHPHPPAFSPAFNLVYWDQDPPERGAPPST 900

QY 901 PKGTPTAENPEYVLGLDVPV 919  
 DB 901 PKGTPTAENPEYVLGLDVPV 919  
 RESULT 3  
 AAW01111  
 ID AAW01111 standard; Protein; 1255 AA.  
 XX AAW01111;  
 AC AAW01111;  
 XX 01-JAN-1997 (first entry)  
 DT 01-JAN-1997 (first entry)  
 XX HER-2/neu protein.  
 DE HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;  
 KW breast cancer; ovary cancer; colon cancer; lung cancer;  
 KW prostate cancer; immunisation; tumour; vaccine; vector.  
 XX Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT 676...1255  
 FT Domain /label= Intracellular\_domain  
 FT /note= "claimed domain, useful for immunisation"  
 XX W09630514-A1.  
 PD 03-OCT-1996.  
 XX 28-MAR-1996; 96WO-US01689.  
 XX 31-MAR-1995; 95US-0414417.  
 XX (UNITW) UNIV WASHINGTON.  
 PA Cheever MA, Disis ML;  
 PI WPI; 1996-455361/45.  
 DR N-PSDB; AAT40739.  
 XX DNA encoding HER-2-neu poly-peptide(s) - used for prevention or  
 PT treatment of malignancies with which the HER-2/neu oncogene is  
 PT associated  
 XX Claim 2; Page 56-61; 71pp; English.  
 PS Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is  
 XX the product of the HER-2/neu oncogene (see also AAT40739). The  
 CC protein is over-expressed in various cancers, including breast,  
 CC ovarian, colon, lung and prostate. The intracellular domain of the  
 CC protein can be used to immunise an animal against malignancy with  
 CC which the oncogene is associated. The polypeptide can be produced  
 CC in transformed host cells for use in immunisation. Alternatively,  
 CC animal cells are transfected in vivo or ex vivo with a viral vector  
 CC that directs expression of the polypeptide.  
 XX Sequence 1255 AA;  
 Query Match 96.5%; Score 4900; DB 17; Length 1255;  
 Best Local Similarity 73.2%; Pred. No. 0;  
 Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
 QY 1 MELALCRWGLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHLYQCQVQGNL 60  
 DB 1 MELALCRWGLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHLYQCQVQGNL 60  
 QY 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIRVGTQLPEDNVALAVLNG 120  
 DB 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIRVGTQLPEDNVALAVLNG 120  
 QY 121 DFLNNTTPTVGASPGCLRELQRLSLEILKGGVLIQRPOLCVQDTILWKDIFHKNQOLA 180

*not about furis*

```
Db 121 DPLNNTTPTVGTASPGGLRELQSLTEILKGGVLIQRNPOLCYQDTILMKDIFHKNNQLA 180
Qy 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCOSLRTVTCAGCARCKGKPLPTDCHEQC 240
Db 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCOSLRTVTCAGCARCKGKPLPTDCHEQC 240
Qy 241 AAGCTGPKHSDCLACILHFNHSGICELHCPALVTYNTDTFESMPNPEGRTYFGASCVTACP 300
Db 241 AAGCTGPKHSDCLACILHFNHSGICELHCPALVTYNTDTFESMPNPEGRTYFGASCVTACP 300
Qy 301 YNYLTDVSGCTVLCPLHNOEVTABDGTQRCCKSPCARVCYGLGMEHLREVRATVSAN 360
Db 301 YNYLTDVSGCTVLCPLHNOEVTABDGTQRCCKSPCARVCYGLGMEHLREVRATVSAN 360
Qy 361 IQBFAGCKTIFGSLAFIPESFDCDASNTAPLOPEQLQVFETLEEITGYLYISAWPDSL 420
Db 361 IQBFAGCKTIFGSLAFIPESFDCDASNTAPLOPEQLQVFETLEEITGYLYISAWPDSL 420
Qy 421 DLSVFQNLQVIRGRIILHNGAYSITLQGLGTSWLGRLSRLRELGSGLALIHNTHLCFVHTV 480
Db 421 DLSVFQNLQVIRGRIILHNGAYSITLQGLGTSWLGRLSRLRELGSGLALIHNTHLCFVHTV 480
Qy 481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPGTQCVCNCSQFLRGQEC 540
Db 481 PWDQLFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPGTQCVCNCSQFLRGQEC 540
Qy 541 VEECRVLQGLPREYVNAHCLPCHPCOPONGSVTCFGEADOCVACAHYKOPPCVAVRC 600
Db 541 VEECRVLQGLPREYVNAHCLPCHPCOPONGSVTCFGEADOCVACAHYKOPPCVAVRC 600
Qy 601 PSQVKPDLSTMPYIWKFPDEBAGCQPCPINCTHSCVDLDDKGCFAEQRASPLTS----- 653
Db 601 PSQVKPDLSTMPYIWKFPDEBAGCQPCPINCTHSCVDLDDKGCFAEQRASPLTSIIISAVVG 660
Qy 654 ----- 653
Db 661 ILLVVVLGVVFGILIKRQOKIRKYTMRLLOETELVEPLTPSGAMPNOAQMRLKETEL 720
Qy 654 ----- 653
Db 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPIVAIKVLRENTSPKANKILDEAYVMAGVGP 780
Qy 654 ----- 653
Db 781 YVSRLLGICITSTVQLVTQMLPYGCLLDHVRENRLGRLSQDILLNWCMIAGKMSYLEDYR 840
Qy 654 ----- 653
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLIDETEYHADGGKVPKMWALESLIRRRFT 900
Qy 654 ----- 653
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPICTIDVYIMVYKWM 960
Qy 654 -----QNEDLGPASPLDSTFYRSLLEDDDDMGDLVA 684
Db 961 IDSECRPRELVSERWARDPQRFVQNEDLGPASPLDSTFYRSLLEDDDDMGDLVA 1020
Qy 685 EYLVVQQGFFCDDPAPGAGMVHHRSSSTRSGGDLTLGLEPSEEBAPRSPAPSEG 744
Db 1021 EYLVVQQGFFCDDPAPGAGMVHHRSSSTRSGGDLTLGLEPSEEBAPRSPAPSEG 1080
Qy 745 AGSDVFDGDLGMAAGLQSLTHDPSPLQRYSEDPVPLPSETDGVAVAPLTCSPQPEV 804
Db 1081 AGSDVFDGDLGMAAGLQSLTHDPSPLQRYSEDPVPLPSETDGVAVAPLTCSPQPEV 1140
Qy 805 NQPDVRFQPPSPREGPLPAARAGATLERPKTLSPCKNGVVKDVFAFGAVENPEYLTQ 864
Db 1141 NQPDVRFQPPSPREGPLPAARAGATLERPKTLSPCKNGVVKDVFAFGAVENPEYLTQ 1200
Qy 865 GGAAPOHPHPPAPSPADNLYWDQDPPPERGAPPSTFKGTPTAENPEYLGLDV 919
Db 1201 GGAAPOHPHPPAPSPADNLYWDQDPPPERGAPPSTFKGTPTAENPEYLGLDV 1255
```

## RESULT 4

AAW92406  
ID AAW92406 standard; Protein; 1255 AA.

XX

AC AAW92406;

XX

DT 21-APR-1999 (first entry)

XX

DE Human HER-2/neu oncogene protein.

XX

KW HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 676..1255

XX

/note= "region which elicits immune response"

XX

PN US9869445-A.

XX

PD 09-FEB-1999.

XX

PF 01-APR-1996; 96US-0625101.

XX

PR 01-APR-1996; 96US-0625101.

XX

PR 17-MAR-1993; 93US-0033644.

XX

PR 12-AUG-1993; 93US-0106112.

XX

PR 31-MAR-1995; 95US-0414417.

XX

PA (UNIW ) UNIV WASHINGTON.

XX

PI Cheever MA, Disis ML;

XX

DR WPI; 1999-152835/13.

XX

DR N-PSDB; AAX01912.

XX

PT Use of HER-2/neu polypeptides - for eliciting an immune response to

XX

PT an HER-2/neu associated malignancy, particularly for treating or

XX

PS Claim 3; Column 31-38; 26pp; English.

XX

CC This sequence represents the human HER-2/neu oncogene protein. A fragment

XX

CC of this protein is used in a method for eliciting or enhancing an immune

XX

CC response to HER-2/neu protein. The polypeptide can stimulate T cells and

XX

CC B cells to produce an immune response to the HER-2/neu protein. The

XX

CC method can be used for immunisation against a malignancy in which the

XX

CC HER-2/neu oncogene is associated and in the treatment of an existing

XX

CC tumour, or to prevent tumour occurrence or reoccurrence.

SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 20; Length 1255;

Best Local Similarity 73.2%; Pred. No. 0;

Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

Qy 1 MELAALCRWGLLLALLPFGAASQVCTGTDMKRLPASPETHLDMRLHYQSCVVQGNL 60

Db 1 MELAALCRWGLLLALLPFGAASQVCTGTDMKRLPASPETHLDMRLHYQSCVVQGNL 60

Qy 61 ELYLPTNASLSFLQDIQEVQGYVLIHNOVRQVPLQRLIRVGRQTQFEDNYALVLDNG 120

Db 61 ELYLPTNASLSFLQDIQEVQGYVLIHNOVRQVPLQRLIRVGRQTQFEDNYALVLDNG 120

Qy 121 DPLNNTTPTVGTASPGGLRELQSLTEILKGGVLIQRNPOLCYQDTILMKDIFHKNNQLA 180

Db 121 DPLNNTTPTVGTASPGGLRELQSLTEILKGGVLIQRNPOLCYQDTILMKDIFHKNNQLA 180

Qy 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCOSLRTVTCAGCARCKGKPLPTDCHEQC 240

Db 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCOSLRTVTCAGCARCKGKPLPTDCHEQC 240



QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
QY 361 IQEFAGCKKI FGSALFPLPSFGDPSASNTAPLQPEQLQVFETLEETIYGLYISAWPDSLP 420  
DB 361 IQEFAGCKKI FGSALFPLPSFGDPSASNTAPLQPEQLQVFETLEETIYGLYISAWPDSLP 420  
QY 421 DLSVFONLQVIRGRIILHNGAYSITLQGLGTSWLGRLSRLSGLALIHNTHLFCFVHTV 480  
DB 421 DLSVFONLQVIRGRIILHNGAYSITLQGLGTSWLGRLSRLSGLALIHNTHLFCFVHTV 480  
QY 481 PWDOLFRNPHOALLHTTANPEDECVEGLACHQLCARGHCWPGPTQCVNCSQFLRGQBC 540  
DB 481 PWDOLFRNPHOALLHTTANPEDECVEGLACHQLCARGHCWPGPTQCVNCSQFLRGQBC 540  
QY 541 VEECRVLQGLPREYVYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VEECRVLQGLPREYVYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSGVKPDLISYMPIWKPEDEGACQPCINCTHSCVDLDDKGCPCAEQASPLTS----- 653  
DB 601 PSGVKPDLISYMPIWKPEDEGACQPCINCTHSCVDLDDKGCPCAEQASPLTSIIISAVVG 660  
QY 654 ----- 653  
DB 661 ILLVVVLGVVFGILLIKRQOKIRKYTMRLLOETELVEPLTPSGAMPNQAQMRILKETEL 720  
QY 654 ----- 653  
DB 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPVAIKVLRENTSFRANKILDEAYVMAGVGP 780  
QY 654 ----- 653  
DB 781 YVSRLLGICLTSTVQLVTQLMPYGCILLDHVNRNRLGSLDLNWCWQIAKMSYLEVDR 840  
QY 654 ----- 653  
DB 841 LVHRDLAARNVLKSPNVKIIDTDFGLARLLDDETEYHADGGKVPKIKWALSILERRFT 900  
QY 654 ----- 653  
DB 901 HQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYIMVKWM 960  
QY 654 -----ONEDLGPASPLDSTFYRSLLDDEDDMGDLVDA 684-  
DB 961 IDSECRPRFRELVSERFARMARDPQRFVVIQNEDLGPASPLDSTFYRSLLDDEDDMGDLVDA 1020  
QY 685 EYLVVQOQGFCCPDAPAGGMVHRRSSSTRSGGDLTLGLEPSEERAPSPAPSEG 744  
DB 1021 EYLVVQOQGFCCPDAPAGGMVHRRSSSTRSGGDLTLGLEPSEERAPSPAPSEG 1080  
QY 745 AGSDVFDGLGMAAGKLSLTHDPSPLQRYSEDTFVLPSETDGYVAPLTCSPQPEYV 804  
DB 1081 AGSDVFDGLGMAAGKLSLTHDPSPLQRYSEDTFVLPSETDGYVAPLTCSPQPEYV 1140  
QY 805 NQPDVFPQPPSPREGPLPAARPAAGATLERPKTLSPGKNGVVKDVPFAGGAVENPEYLTPO 864  
DB 1141 NQPDVFPQPPSPREGPLPAARPAAGATLERPKTLSPGKNGVVKDVPFAGGAVENPEYLTPO 1200  
QY 865 GGAAPQHPHPPAFSPADNLYWDDQPPBERGAPPSTFKGTPTAENPEYLGLODVPV 919  
DB 1201 GGAAPQHPHPPAFSPADNLYWDDQPPBERGAPPSTFKGTPTAENPEYLGLODVPV 1255

RESULT 6

AAY84780

ID AAY84780 standard; Protein; 1255 AA.

XX

AC AAY84780;

XX

DT 08-AUG-2000 (first entry)

XX Amino acid sequence of the SPLICE erbB-2 receptor protein.  
DE SPLICE erbB-2 receptor protein; cell transformation disorder; cancer;  
XX tumor cell proliferation; tissue degeneration; arthropathy;  
KW bone resorption; inflammatory disease; degenerative disorder;  
KW wound healing.  
XX Homo sapiens.  
OS WO200020579-A1.  
PN 13-APR-2000.  
XX 01-OCT-1999; 99WO-CA00912.  
XX 02-OCT-1998; 98US-0165192.  
XX (UYMC-) UNIV MCMASTER.  
PI Muller WJ, Siegel PW;  
XX WPI; 2000-303768/26.  
DR N-PSDB; AAA14812.  
XX Nucleic acid encoding an erbB 2 receptor protein designated SPLICE  
erbB-2, inhibitors of the protein are useful for treatment of cancer -  
Claim 3; Fig 2; 60pp; English.

The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.

SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 21; Length 1255;

Best Local Similarity 73.2%; Pred. No. 0;

Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHYQCGVQVQNL 60

DB 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHYQCGVQVQNL 60

QY 61 ELTYLPTNASLSFLQDIEVQGYVLIHNVQRPVQLRLIRVGTQLPEDNALAVLDNG 120

DB 61 ELTYLPTNASLSFLQDIEVQGYVLIHNVQRPVQLRLIRVGTQLPEDNALAVLDNG 120

QY 121 DPLNNTPTVGTASPGGLRELQRLSRLTEILKGVLIQRNPOLCYQDTILWKDIFHKNNQLA 180

DB 121 DPLNNTPTVGTASPGGLRELQRLSRLTEILKGVLIQRNPOLCYQDTILWKDIFHKNNQLA 180

QY 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSILTRTVACGGCARCKGLPTDCCHEQC 240

DB 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSILTRTVACGGCARCKGLPTDCCHEQC 240

QY 241 AAGCTGPKHSDCLACLFHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300

DB 241 AAGCTGPKHSDCLACLFHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300

QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360

DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360







QY 361 IQEFACKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLBEITGYLYTISAWPDSLP 420  
 Db 361 IQEFACKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLBEITGYLYTISAWPDSLP 420  
 QY 421 DLSVFQNLQVIRGRILHNGAYSITLQGLGISWGLRSLRELGLALIHNNTHLCFVHTV 480  
 Db 421 DLSVFQNLQVIRGRILHNGAYSITLQGLGISWGLRSLRELGLALIHNNTHLCFVHTV 480  
 QY 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHQLCARGHCWGPPTQCVCNCSQFLRGQBC 540  
 Db 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHQLCARGHCWGPPTQCVCNCSQFLRGQBC 540  
 QY 541 VBECRVLQGLPREYNARHCLPCHPECQPNQSGVTCFGEADQCACAHYKDPFPCVARC 600  
 Db 541 VBECRVLQGLPREYNARHCLPCHPECQPNQSGVTCFGEADQCACAHYKDPFPCVARC 600  
 QY 601 PSQVAPDLSYMPFWKPPDEEGACQPCINCTHSCVDLDDKGPAPORASPLTS 653  
 Db 601 PSQVAPDLSYMPFWKPPDEEGACQPCINCTHSCVDLDDKGPAPORASPLTS 653  
 QY 654 654 653  
 Db 661 ILLVVVLGVVGLIKRQOKIRKYTMRELLQETELVEPLTPSGAMPNQAMRILKETEL 720  
 QY 654 654 653  
 Db 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVAGVSP 780  
 QY 654 654 653  
 Db 781 YVSRLLGICLTSTVOLVTLQMPYGLLDHVRNRRGLSGDILLNMCQIAKMSYLEDRV 840  
 QY 654 654 653  
 Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGCKVPIKWMALLESILRRFT 900  
 QY 654 654 653  
 Db 901 HQSDVMSYGVTVWELMTFGAKPYDGIPIAREIPOLLEKGBRLPQPICTIDVTYIMVKWM 960  
 QY 654 654 653  
 Db 961 IDSECRPRFRELVSFMRWARDPQFVVIQNEEDLGPASPLDSTFYRSLLDDDDMDGLVDA 1020  
 QY 685 BEYLVPOQFFCPDPAGAGVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEG 744  
 Db 1021 BEYLVPOQFFCPDPAGAGVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEG 1080  
 QY 745 AGSDVFDGDLGMAAGLQSLPHTDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEV 804  
 Db 1081 AGSDVFDGDLGMAAGLQSLPHTDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEV 1140  
 QY 805 NQPDVRPQPPSPREGPLPAARPAGATLBRPKTLSPGKNGVVKDVPAGAVENPYLTPQ 864  
 Db 1141 NQPDVRPQPPSPREGPLPAARPAGATLBRPKTLSPGKNGVVKDVPAGAVENPYLTPQ 1200  
 QY 865 GGAAPQPPPPAFSPFNLYWQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919  
 Db 1201 GGAAPQPPPPAFSPFNLYWQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255

RESULT 9

AAE24067  
 ID AAE24067 standard; Protein; 1255 AA.  
 AC AAE24067;  
 DT 23-SEP-2002 (first entry)  
 DE Human Her-2 protein.  
 XX Human; Her-2; epidermal growth factor receptor 2; infection; cancer;  
 KW hyperproliferative disorder; prophylaxis; inflammation; antisense;  
 QY

KW tumour; gene therapy; phosphorothioate backbone.  
 OS Homo sapiens.  
 XX WO200222636-A1.  
 XX 21-MAR-2002.  
 XX 12-SEP-2001; 2001WO-US28572.  
 XX 15-SEP-2000; 2000US-0663834.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Bennett CF, Cowseert LM;  
 XX WPI: 2002-471192/50.  
 XX N-PSDB; AAD38904.  
 PT Novel antisense oligonucleotide which modulates the expression of Human  
 PT Epidermal Growth Factor receptor, Her2, is useful for treating tumors  
 PT inflammation or to prevent infection in humans -  
 XX Example 13; Page 95-107; 116pp; English.  
 CC The invention relates to antisense compounds targeted to a nucleic  
 CC acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2)  
 CC that specifically hybridises with and inhibits the expression of Her2.  
 CC Antisense compounds of the invention are used for treating diseases or  
 CC conditions associated with Her2 such as hyperproliferative disorders  
 CC e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary,  
 CC neural or cardiac cancer. They are also useful prophylactically e.g.  
 CC to prevent or delay infection, inflammation and tumour formation. The  
 CC invention is also used in gene therapy. The present sequence is human  
 CC Her-2 protein.  
 XX SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;  
 Best Local Similarity 73.2%; Pred. No. 0;  
 Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLLALLPFGAASSTQVCTCTDMKRLPASPETHLDMRLHYQSCVQVQNL 60  
 Db 1 MELAALCRWGLLLALLPFGAASSTQVCTCTDMKRLPASPETHLDMRLHYQSCVQVQNL 60  
 QY 61 ELTYLPTNASLFLQDIQEVQGVYLIHNVQRPVLPQRLRIVRGTLQFEDNYALAVLNG 120  
 Db 61 ELTYLPTNASLFLQDIQEVQGVYLIHNVQRPVLPQRLRIVRGTLQFEDNYALAVLNG 120  
 QY 121 DPLNNTTPTVTCASPGGLRELOLRSITLTKGVLIQRNPOLCYQDTILWKDIFHKNQOLA 180  
 Db 121 DPLNNTTPTVTCASPGGLRELOLRSITLTKGVLIQRNPOLCYQDTILWKDIFHKNQOLA 180  
 QY 181 LTLIDTNRSRACHPCSPMKGSRWCSESDCQSLTRTVACGACRCKGPLTDCCHQC 240  
 Db 181 LTLIDTNRSRACHPCSPMKGSRWCSESDCQSLTRTVACGACRCKGPLTDCCHQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGYTFGASCVTACP 300  
 Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHNVQVTAEDGTQRCCKSPKPCARVCYIGMGHLEHREAVTSAN 360  
 Db 301 YNYLSTDVGSCTLVCPHNVQVTAEDGTQRCCKSPKPCARVCYIGMGHLEHREAVTSAN 360  
 QY 361 IQEFACKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLBEITGYLYTISAWPDSLP 420  
 Db 361 IQEFACKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLBEITGYLYTISAWPDSLP 420  
 QY 421 DLSVFQNLQVIRGRILHNGAYSITLQGLGISWGLRSLRELGLALIHNNTHLCFVHTV 480  
 Db 421 DLSVFQNLQVIRGRILHNGAYSITLQGLGISWGLRSLRELGLALIHNNTHLCFVHTV 480

QY 481 PWDQFRNPHQALLHTANRPEDECVEGLACHQLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
Db 481 PWDQFRNPHQALLHTANRPEDECVEGLACHQLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
QY 541 VBECRVLQGLPREYVNAHCLPCHPBCQPNQSGSVTCFGEADQCACAHYKDPKPPFCVARC 600  
Db 541 VBECRVLQGLPREYVNAHCLPCHPBCQPNQSGSVTCFGEADQCACAHYKDPKPPFCVARC 600  
QY 601 PSVKEDLSVMTKPEDEGACQPCINCTHSCVDLDDKGCFAEORASPLTS----- 653  
Db 601 PSVKEDLSVMTKPEDEGACQPCINCTHSCVDLDDKGCFAEORASPLTSIIISAVVG 660  
QY 654 ----- 653  
Db 661 ILLVVVLGVVGLIKERQKIRKYTMRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
QY 654 ----- 653  
Db 721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRNTPSKANKELDEAYVMAGVGSF 780  
QY 654 ----- 653  
Db 781 YVSRLLGICLTSTVQLVLTQMPVGLLDHVRENRLGSGDILLNWCMTAKGMSYLEDVR 840  
QY 654 ----- 653  
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKMWALBSILLRRFT 900  
QY 654 ----- 653  
Db 901 HQSDVMSYGVVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPPICTTIDVYIMVKWM 960  
QY 654 ----- 653  
Db 961 IDSECRPRFRELVSFERSMARDPQRFVWTONEDLGPASPLDSTFYKSLLEDMDGLVDA 1020  
QY 685 EYLVVQOQFFCPDPAPAGAGVHHRSSVTRSGGGDLTLGLEPSEEAAPRSLAPSG 744  
Db 1021 EYLVVQOQFFCPDPAPAGAGVHHRSSVTRSGGGDLTLGLEPSEEAAPRSLAPSG 1080  
QY 745 AGSDVFDGLGMAAGLQSLPHTDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 804  
Db 1081 AGSDVFDGLGMAAGLQSLPHTDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140  
QY 805 NQPDVFPQPPSPREGPLPAARPAAGATLERPKTLSPCKNGVWVDVFAFGAVENPEYLTQ 864  
Db 1141 NQPDVFPQPPSPREGPLPAARPAAGATLERPKTLSPCKNGVWVDVFAFGAVENPEYLTQ 1200  
QY 865 GGAAPQPPPPAFSPAFDNLVYWDQPPPERGAPPSTFKGTPTAENPEYLGLDVVPV 919  
Db 1201 GGAAPQPPPPAFSPAFDNLVYWDQPPPERGAPPSTFKGTPTAENPEYLGLDVVPV 1255

RESULT 10  
AAE20479  
ID AAE20479 standard; Protein; 1255 AA.  
AC AAE20479;  
DT 01-JUL-2002 (first entry)  
XX Human Her-2/neu protein.  
DE Human, Her-2/Neu protein; immune response; gene therapy; breast cancer;  
KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1021..1030  
FT Region  
FT /note= "Naturally processed HLA-B44-restricted epitope"  
XX

PN WO200214503-A2.  
XX 21-FEB-2002.  
XX 14-AUG-2001; 2001WO-US41733.  
XX 14-AUG-2000; 2000US-225152P.  
PR 28-SEP-2000; 2000US-236428P.  
PR 21-FEB-2001; 2001US-270520P.  
XX (CORI-) CORIXA CORP.  
PA Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
XX McNeill PD, Vedwick TS;  
PI WPI; 2002-280758/32.  
XX N-PSDB; AAD32743.  
DR DR  
XX Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
PT prevention and diagnosis of cancer, preferably breast cancer -  
XX Disclosure; Page 114-117; 129pp; English.  
XX The invention relates to an isolated Her-2/Neu polypeptide composition  
CC effective for eliciting an immune response. The invention is useful for  
CC eliciting an immune response in a patient, where the patient is human  
CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
CC The composition is useful for the therapy and diagnosis of cancer,  
CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
CC and other compositions for the diagnosis, prevention and treatment of  
CC human malignancies, for stimulating and/or expanding T cells specific for  
CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a  
CC patient. The invention is useful for stimulating a T cell response in a  
CC human patient, as probe or primer for nucleic acid hybridisation, to  
CC selectively form duplex molecules with complementary stretches of the  
CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full  
CC length gene from a suitable library, and to direct expression of a  
CC polypeptide in appropriate host cells. The composition is useful in  
CC prophylactic or therapeutic applications and for the treatment of cancer,  
CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
CC associated malignancies. The invention is useful in gene therapy. The  
CC present sequence is human Her-2/neu protein.  
XX Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;  
Best Local Similarity 73.2%; Pred. No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPFGAASQVCTGTMKRLPASPETHLDMRLHYQGCVVQGNL 60  
Db 1 MELAALCRWGLLLALLPFGAASQVCTGTMKRLPASPETHLDMRLHYQGCVVQGNL 60  
QY 61 ELTYLPTNASLFLQDIQEVQGVLIHNVQVFLORLIRVGTQLFEDNALAVLDNG 120  
Db 61 ELTYLPTNASLFLQDIQEVQGVLIHNVQVFLORLIRVGTQLFEDNALAVLDNG 120  
QY 121 DPLNNTTPTVGTASPGGLRELQRLSITELKGVLIQORNPOLCYQDTILWKDIFHKNNOLA 180  
Db 121 DPLNNTTPTVGTASPGGLRELQRLSITELKGVLIQORNPOLCYQDTILWKDIFHKNNOLA 180  
QY 181 LTLIDTNRSRACHPCSPMKGSRGWESSEDQSLTRTVTCAGGCARCKPLPTDCHEQC 240  
Db 181 LTLIDTNRSRACHPCSPMKGSRGWESSEDQSLTRTVTCAGGCARCKPLPTDCHEQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCYTAC 300  
Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCYTAC 300  
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSPCARVCYGLGMEHLREVRVTSAN 360  
Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSPCARVCYGLGMEHLREVRVTSAN 360

```
QY 361 IOEFAGCKKIFGSLAFAPLBPESFGDPASNTAPLOPEQLQVFFTEITGLYIYISAWPDSLP 420
Db 361 IOEFAGCKKIFGSLAFAPLBPESFGDPASNTAPLOPEQLQVFFTEITGLYIYISAWPDSLP 420
QY 421 DLSVFQNLQVIRGRILHNCAYSLTQGLGISWLGRLSRELGSGLALHNNTHLCFVHTV 480
Db 421 DLSVFQNLQVIRGRILHNCAYSLTQGLGISWLGRLSRELGSGLALHNNTHLCFVHTV 480
QY 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHQLCARGHCWGPPTQCVCNCSQFLRGQEC 540
Db 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHQLCARGHCWGPPTQCVCNCSQFLRGQEC 540
QY 541 VEECRVLOGLPREYNARHCLPCHPECOFONGSVTCFGEADQCACAHYKDPDPFCVARC 600
Db 541 VEECRVLOGLPREYNARHCLPCHPECOFONGSVTCFGEADQCACAHYKDPDPFCVARC 600
QY 601 PSGVKPDLISYMPIWKFPPDEEGACQPCINCHTSCVDLDDKGCFAORASPLTS 653
Db 601 PSGVKPDLISYMPIWKFPPDEEGACQPCINCHTSCVDLDDKGCFAORASPLTS 653
QY 654 ----- 653
Db 654 ----- 653
QY 661 ILLVVVLGVVFGILLIKRQOKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720
Db 661 ILLVVVLGVVFGILLIKRQOKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720
QY 654 ----- 653
Db 654 ----- 653
QY 721 RKVVLGSGAGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVSP 780
Db 721 RKVVLGSGAGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVSP 780
QY 654 ----- 653
Db 654 ----- 653
QY 781 YVSRLLGICLTSTVQLTQMPYGCGLDVRNRCGLSGQDLLANCMQIAKMSYLEDVR 840
Db 781 YVSRLLGICLTSTVQLTQMPYGCGLDVRNRCGLSGQDLLANCMQIAKMSYLEDVR 840
QY 654 ----- 653
Db 654 ----- 653
QY 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKGVPIKMALESILRRFT 900
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKGVPIKMALESILRRFT 900
QY 654 ----- 653
Db 654 ----- 653
QY 901 HQSDVMSYGVTVWELMTGAKPYDGIPIAREIPDLLEKGERLPPOPICTIDVYMIWVKWM 960
Db 901 HQSDVMSYGVTVWELMTGAKPYDGIPIAREIPDLLEKGERLPPOPICTIDVYMIWVKWM 960
QY 654 ----- 653
Db 654 ----- 653
QY 961 IDSECRPRFRELVSFSEARMARDPQRFVQINEDLGPASPLDSTFYRSLEDDDMGDLYDA 1020
Db 961 IDSECRPRFRELVSFSEARMARDPQRFVQINEDLGPASPLDSTFYRSLEDDDMGDLYDA 1020
QY 685 ERYLVPQOGFFCPDPAPGAGGVHHRSSSTRSGGDLTLGLEPSEBAPRSLAPSEG 744
Db 1021 ERYLVPQOGFFCPDPAPGAGGVHHRSSSTRSGGDLTLGLEPSEBAPRSLAPSEG 1080
QY 745 AGSDVFDGDLGMAAGLQSLPHTDPSPLQRYSEDTVPLPSETDGYVAPLTCSPQPEYV 804
Db 1081 AGSDVFDGDLGMAAGLQSLPHTDPSPLQRYSEDTVPLPSETDGYVAPLTCSPQPEYV 1140
QY 805 NQPDVRPQPPSPREGFLPAARPAAGATLBRPRTLSPGKNGVVKDVPAGGAVENPBYLTPQ 864
Db 1141 NQPDVRPQPPSPREGFLPAARPAAGATLBRPRTLSPGKNGVVKDVPAGGAVENPBYLTPQ 1200
QY 865 GGAAPQHPHPPAFSAFONLYWDDQPPERGAPPSTFKGTPTAENPEYLGDDVPV 919
Db 1201 GGAAPQHPHPPAFSAFONLYWDDQPPERGAPPSTFKGTPTAENPEYLGDDVPV 1255
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## RESULT 11

AAM51143

ID AAM51143 standard; Protein; 1255 AA.

XX AC AAM51143;

DT 17-JUN-2002 (first entry)

DE Human Her-2/neu oncogene-encoded p185 glycoprotein.

KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
tyrosine kinase; receptor; c-erbB2; gene therapy.

```
XX Homo sapiens.
OS 1. 653
FH Key Location/Qualifiers
FT Domain /note= "extracellular domain"
FT Domain /note= "intracellular domain"
FT Domain /note= "phosphorylation domain"
XX WO200212341-A2.
XX 14-FEB-2002.
XX 03-AUG-2001; 2001WO-US24283.
XX 03-AUG-2000; 2000US-0632507.
XX (CORI-) CORIXA CORP.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX Cheever MA, Gheysen D;
XX WPI; 2002-241743/29.
XX N-PSDB; ABA92250.
XX Her-2/neu fusion protein for treating or preventing cancer by eliciting
or enhancing an immune response to the protein. has Her-2/neu
extracellular domain fused to Her-2/neu intracellular or
phosphorylation domain
XX Claim 68; Fig 7; 141pp; English.
XX The present sequence is that of human Her-2/neu (p185 glycoprotein
or c-erbB2), an oncogenic self-protein and target for anti-cancer
vaccines. The Her-2/neu gene is amplified and p185 is overexpressed
in a variety of cancers, including breast, ovarian, colon, lung and
prostate cancer. Her-2/neu is a member of the tyrosine kinase
family of receptor-like glycoproteins. It comprises an extracellular
domain with homology to the epidermal growth factor receptor
(EGFR), a highly hydrophobic transmembrane domain and a C-terminal
intracellular domain that also shows homology to EGFR. Its
overexpression correlates with a poor prognosis in breast and
ovarian cancers. The invention provides Her-2/neu fusion
proteins, nucleic acids encoding them, viral vectors, and vaccines
comprising the fusion proteins or nucleic acid molecules. In
preferred fusion proteins, the extracellular domain of a Her-2/neu
protein is fused to a Her-2/neu intracellular domain or
phosphorylation domain (or its DeltaPD fragment). An immune
response to Her-2/neu protein is elicited or enhanced by
administering the fusion protein in the form of a vaccine, or by
transfecting cells of an animal ex vivo with a nucleic acid
encoding the fusion protein, and delivering the transfected cells
to the animal. The fusion proteins, nucleic acids, and isolated
specific T-cells are useful for inhibiting the development of a
cancer, especially breast, ovarian, colon, lung or prostate cancer
in a patient. T cells that specifically react with a Her-2/neu
fusion protein can be used to remove tumour cells from a sample in
order to inhibit the development of cancer in a patient.
```

XX Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;

Best Local Similarity 73.2%; Pred. No. 0;

Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLLALLPFGAASVCTGTDKMLRPLASPETHLDMRLHYQCQVQGNL 60

Db 1 MELAALCRWGLLLALLPFGAASVCTGTDKMLRPLASPETHLDMRLHYQCQVQGNL 60

QY 61 ELTYLPTNASTLFLQDIOEVQGYVLIAHNQVQVPLQRLVRGTFQDPEDNYALVDNG 120

Db 61 ELTYLPTNASLFLQDIOEVQGVLIHQAQVQVPLQRLIRVGTQLFEDNVALAVLNG 120  
 QY 121 DPLNNTPTVGTASPGGLRELQSLRTEILKGGVLIQORNQVLCYQDTILWKDIFHKNQLA 180  
 Db 121 DPLNNTPTVGTASPGGLRELQSLRTEILKGGVLIQORNQVLCYQDTILWKDIFHKNQLA 180  
 QY 181 LTLIDNTRSRACHPCSPMKGRCWGESSEDCQSLTRTVACGACRCKGPLPTDCHEOC 240  
 Db 181 LTLIDNTRSRACHPCSPMKGRCWGESSEDCQSLTRTVACGACRCKGPLPTDCHEOC 240  
 QY 241 AGCTGPKHSDCLACHFNHSGICELHPCALVYNTDTESMPNPEGRVTFGASCVTACP 300  
 Db 241 AGCTGPKHSDCLACHFNHSGICELHPCALVYNTDTESMPNPEGRVTFGASCVTACP 300  
 QY 301 YNVLSTDVGSCTLVCPHNOEVTAEQGTORCEKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 Db 301 YNVLSTDVGSCTLVCPHNOEVTAEQGTORCEKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 QY 361 IQEFAGCKKIFGSLAFPLPESFDGDPASNTAPLQPEQLQVFETLEETIGYLYISAMPDSL 420  
 Db 361 IQEFAGCKKIFGSLAFPLPESFDGDPASNTAPLQPEQLQVFETLEETIGYLYISAMPDSL 420  
 QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGSLGLRSRLRELSGLALIHNTLHLCFVHTV 480  
 Db 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGSLGLRSRLRELSGLALIHNTLHLCFVHTV 480  
 QY 481 PWDOLFPRNPHOALLHTANRPEBCEVGEGLACHQLCARGHCWPGPTQCVNCSQFIRGQBC 540  
 Db 481 PWDOLFPRNPHOALLHTANRPEBCEVGEGLACHQLCARGHCWPGPTQCVNCSQFIRGQBC 540  
 QY 541 VEECRVQLQPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPFCVAC 600  
 Db 541 VEECRVQLQPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPFCVAC 600  
 QY 601 PSGVKPDLSPYMPWKFPDEBEGACQPCINCTHSCVDLDDKGCPCAEORASPLTS 653  
 Db 601 PSGVKPDLSPYMPWKFPDEBEGACQPCINCTHSCVDLDDKGCPCAEORASPLTS 653  
 QY 654 ----- 653  
 Db 661 ILLVVLGVVFGILIKRQOKIRKYMRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720  
 QY 654 ----- 653  
 Db 721 RKVKVLGSAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPRANKBELDEAYVMAGVGP 780  
 QY 654 ----- 653  
 Db 781 YVSRLLGICLTSTVQLVQTMYPYGLLDHVRNRRGLSGQDLNWCQIAKGMVSYLEDVR 840  
 QY 654 ----- 653  
 Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKVMALLESILRRRT 900  
 QY 654 ----- 653  
 Db 901 HQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICITIDVYIMVKWM 960  
 QY 654 ----- 653  
 Db 961 IDSECRPRFRELVSFEFSRMARDPQREVVITQNEIDLGPASPLDSTFYRSLLEDDDMGLVDA 1020  
 QY 685 EYLVVQCGFFCPDPAPGAGVHHRSSSTRSGGDLTLGLEPSEEAAPSPAPSE 744  
 Db 1021 EYLVVQCGFFCPDPAPGAGVHHRSSSTRSGGDLTLGLEPSEEAAPSPAPSE 1080  
 QY 745 AGSDVFDGLGMAAGLQSLPHTDPSPLQRYSEDPTVPLPSTDCGYVAPLTCSPQPEYV 804  
 Db 1081 AGSDVFDGLGMAAGLQSLPHTDPSPLQRYSEDPTVPLPSTDCGYVAPLTCSPQPEYV 1140  
 QY 805 NQPDVFPQPPSPREGPLPAARPAATLERPKTLSPGKNGVVKDVFAGGAVENPEYLTQ 864  
 Db 1141 NQPDVFPQPPSPREGPLPAARPAATLERPKTLSPGKNGVVKDVFAGGAVENPEYLTQ 1200

QY 865 GGAAPQPHPPAFSPAFNLVYWDODPPERGAPPSTFKGTPTAENPEYLGLDVPV 919  
 Db 1201 GGAAPQPHPPAFSPAFNLVYWDODPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255

RESULT 12  
 AAU77114

ID AAU77114 standard; Protein; 1255 AA.

XX AAU77114;

DT 05-JUN-2002 (first entry)

XX Human Her-2/neu polypeptide.

XX Human; Her-2/neu; cytostatic; haematological malignancy; CML;

KW acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;

KW chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;

XX Hodgkin's lymphoma; T cell therapy.

XX Homo sapiens.

XX WO200213847-A2.

XX 21-FEB-2002.

PF 13-AUG-2001; 2001WO-US25408.

XX 14-AUG-2000; 2000US-0638280.

PR 28-SEP-2000; 2000US-0675904.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Cheever WA, Hand-zimmermann S;

DR WPI; 2002-280741/32.

DR N-PSDB; ABK10730.

XX Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide encoding the polypeptide, or antigen presenting cells expressing the polypeptide

XX Disclosure; Page 71-74; 74pp; English.

XX The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polynucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.

XX Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;

Best Local Similarity 73.2%; Pred. No. 0;

Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLLALLPFGAASQVCTGTDMLRLPASPEHLDMLRHLYQGVVQGNL 60

Db 1 MELAALCRWGLLLALLPFGAASQVCTGTDMLRLPASPEHLDMLRHLYQGVVQGNL 60

QY 61 ELTYLPTNASLFLQDIOEVQGVLIHQAQVQVPLQRLIRVGTQLFEDNVALAVLNG 120

Db 61 ELTYLPTNASLFLQDIOEVQGVLIHQAQVQVPLQRLIRVGTQLFEDNVALAVLNG 120

QY 121 DPLNNTPTVGTASPGGLRELQSLRTEILKGGVLIQORNQVLCYQDTILWKDIFHKNQLA 180

Db 121 DPLNNTPTVGTASPGGLRELQSLRTEILKGGVLIQORNQVLCYQDTILWKDIFHKNQLA 180

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QY 181 LTLIDNRSRACHPCSPMCKGSRMGESSEDCQSLTRTVACGACRCKGPLPTDCCHEQC 240
Db 181 LTLIDNRSRACHPCSPMCKGSRMGESSEDCQSLTRTVACGACRCKGPLPTDCCHEQC 240
QY 241 AAGCTGPKHSDCLACHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300
Db 241 AAGCTGPKHSDCLACHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300
QY 301 YNYLSTDVGSCTLVCPHNOEVTABDGTQRCBKSKPCARVCYGLCMEHLRVRVAVTSAN 360
Db 301 YNYLSTDVGSCTLVCPHNOEVTABDGTQRCBKSKPCARVCYGLCMEHLRVRVAVTSAN 360
QY 361 IQEFAGCKKIFGSLAPLPSFGDPSANTAPLQPEQLQVFETLEBITGYLISAWPDSL 420
Db 361 IQEFAGCKKIFGSLAPLPSFGDPSANTAPLQPEQLQVFETLEBITGYLISAWPDSL 420
QY 421 DLSVFQNLQVIRGRIHNGAYSLTQGLGISWGLRSRELGSGLALIHNNTHLCFVHTV 480
Db 421 DLSVFQNLQVIRGRIHNGAYSLTQGLGISWGLRSRELGSGLALIHNNTHLCFVHTV 480
QY 481 PWDQLFRPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQEC 540
Db 481 PWDQLFRPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQEC 540
QY 541 VEECRVLOGLPREYVYVNRHCLPCHPECOQPONGSVTCFGEADQCVACAHYKDPPEFCVARC 600
Db 541 VEECRVLOGLPREYVYVNRHCLPCHPECOQPONGSVTCFGEADQCVACAHYKDPPEFCVARC 600
QY 601 PSGVKPDLISYMPIWKFPEDEGACQCPNCTHSCVDLDDKGPAPQASPLTS----- 653
Db 601 PSGVKPDLISYMPIWKFPEDEGACQCPNCTHSCVDLDDKGPAPQASPLTS----- 653
QY 654 ----- 653
Db 654 ----- 653
QY 661 ILLVVVLGVVFGILLIKRQOKIRKYMRLLOETELVEPLTPSGAMPNQAOQMRILKETEL 720
Db 661 ILLVVVLGVVFGILLIKRQOKIRKYMRLLOETELVEPLTPSGAMPNQAOQMRILKETEL 720
QY 654 ----- 653
Db 654 ----- 653
QY 721 RKVKVLGSGAGTVYKGIWIPGENVKIPVALKVLRENTSPKANKEILDEAYVMAGVSP 780
Db 721 RKVKVLGSGAGTVYKGIWIPGENVKIPVALKVLRENTSPKANKEILDEAYVMAGVSP 780
QY 654 ----- 653
Db 654 ----- 653
QY 781 YVSRLLGHICLTSTVQLVTLQMPYGLCLDHRNRRGLSGQDLLNWCMTAKGMSYLEDVR 840
Db 781 YVSRLLGHICLTSTVQLVTLQMPYGLCLDHRNRRGLSGQDLLNWCMTAKGMSYLEDVR 840
QY 654 ----- 653
Db 654 ----- 653
QY 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKIMWALESIILRRFT 900
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKIMWALESIILRRFT 900
QY 654 ----- 653
Db 654 ----- 653
QY 901 HQSDVMSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICTIDVYIMVCKWM 960
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICTIDVYIMVCKWM 960
QY 654 ----- 653
Db 654 ----- 653
QY 961 IDSECRPRFRELVSFSEFMRARDPQRFVVTQNEDLGPASPLDSTFYRSLLEDDMDGLVDA 1020
Db 961 IDSECRPRFRELVSFSEFMRARDPQRFVVTQNEDLGPASPLDSTFYRSLLEDDMDGLVDA 1020
QY 685 EYLVPQGGFCFDPAPGAGGVHRRHSSSTRSGGDLTLGLEPSEEA PRSLAPSEG 744
Db 685 EYLVPQGGFCFDPAPGAGGVHRRHSSSTRSGGDLTLGLEPSEEA PRSLAPSEG 744
QY 1021 EYLVPQGGFCFDPAPGAGGVHRRHSSSTRSGGDLTLGLEPSEEA PRSLAPSEG 1080
Db 1021 EYLVPQGGFCFDPAPGAGGVHRRHSSSTRSGGDLTLGLEPSEEA PRSLAPSEG 1080
QY 745 AGSDVFDGDLGMAAKGLQSLPTHPDPSLQRYSEDTVPLPSETDGYVAPLTCSPQPYV 804
Db 745 AGSDVFDGDLGMAAKGLQSLPTHPDPSLQRYSEDTVPLPSETDGYVAPLTCSPQPYV 804
QY 1081 AGSDVFDGDLGMAAKGLQSLPTHPDPSLQRYSEDTVPLPSETDGYVAPLTCSPQPYV 1140
Db 1081 AGSDVFDGDLGMAAKGLQSLPTHPDPSLQRYSEDTVPLPSETDGYVAPLTCSPQPYV 1140
QY 805 NQPDVRPQPPSPREGPLPAARPAAGATLERPKTSLPGKNGVKDVAFGCAVENPEYLPQ 864
Db 805 NQPDVRPQPPSPREGPLPAARPAAGATLERPKTSLPGKNGVKDVAFGCAVENPEYLPQ 864
QY 1141 NQPDVRPQPPSPREGPLPAARPAAGATLERPKTSLPGKNGVKDVAFGCAVENPEYLPQ 1200
Db 1141 NQPDVRPQPPSPREGPLPAARPAAGATLERPKTSLPGKNGVKDVAFGCAVENPEYLPQ 1200
QY 865 GGAAPQHPHPPAFSPFNLYWDDPPERGAPSTFKGTATENPEYLGLDVVP 919
Db 865 GGAAPQHPHPPAFSPFNLYWDDPPERGAPSTFKGTATENPEYLGLDVVP 919
QY 1201 GGAAPQHPHPPAFSPFNLYWDDPPERGAPSTFKGTATENPEYLGLDVVP 1255
Db 1201 GGAAPQHPHPPAFSPFNLYWDDPPERGAPSTFKGTATENPEYLGLDVVP 1255
```

RESULT 13  
AA92620  
ID AA92620 standard; Protein; 1255 AA.  
XX"  
AC AA92620;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Human herregulin 2 (Her2).  
XX  
KW Herregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity;  
KW self-protein; cancer; breast cancer; prostate cancer;  
KW cell-associated peptide antigen; foreign epitope.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 1..173  
FT /label= N-terminal  
FT /note= "mature polypeptide"  
FT Region 5..25  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 59..73  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 103..117  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 149..163  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Domain 174..323  
FT /label= Cysteine\_rich\_domain  
FT Region 210..224  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 250..264  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Domain 324..483  
FT /label= Ligand\_binding\_domain  
FT Region 325..339  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 369..383  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 465..479  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Domain 484..623  
FT /label= Cysteine\_rich\_domain  
FT Region 579..593  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Domain 624..654  
FT /label= Transmembrane\_domain  
FT Region 632..652  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 653..667  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Domain 655..1010  
FT /label= Tyrosine\_kinase\_domain  
FT Region 661..675  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"  
FT Region 695..709  
FT /label= insertion region  
FT /note= "suitable for foreign epitope insertion"



Region 710..730  
 /label= insertion\_region  
 /note= "suitable for foreign epitope insertion"  
 101..1235  
 /label= C-terminal\_domain

XX WO200020027-A2.  
 XX 13-APR-2000.  
 XX 05-OCT-1999; 99WO-DK00525.  
 XX 05-OCT-1998; 98DK-0001261.  
 XX 20-OCT-1998; 98US-0105011.  
 XX (MEBI-) M & E BIOTECH AS.  
 XX Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
 PI Gautam A, Birk P, Karlsson G;  
 XX WPI; 2000-349917/30.  
 DR N-PSDB; AAA09455.  
 XX Inducing immune responses to weakly immunogenic, tumor associated  
 PT peptide antigens for the treatment of breast and prostate cancer  
 XX Claim 62; Page 193-198; 220pp; English.

XX This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of  
 CC Her2 can be used in the claimed method as an autovaccine to induce a CTL  
 CC response. Subdominant CTL epitopes, antibody binding regions and  
 CC cysteine residues involved in disulfide bonds are preserved in the  
 CC immunogenized forms. Regions suitable for the insertion of foreign T  
 CC helper epitopes were identified (see features table). The method  
 CC is used for inducing immune responses against weakly immunogenic  
 CC cell-associated peptide antigens (PA) such as those associated with  
 CC cancers (self-proteins), e.g. human prostate specific membrane antigen  
 CC (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).  
 CC The method comprises effecting simultaneous presentation by antigen  
 CC producing cells (APCs) of the animals immune system of: (1) at least 1  
 CC CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1  
 CC B-cell group derived from the cell-associated PA; and (2) at least 1  
 CC first T helper cell group which is foreign to the animal. Analogues of  
 CC human PSM, human Her2 and human/murine FGF8b comprising a substantial  
 CC part of all known and predicted CTL and B-cell epitopes of the respective  
 CC PA and including at least one foreign T helper epitope are also claimed.  
 CC The method is used to treat prostate, prostate/breast or breast cancer  
 CC when the PA is human PSM, FGF8b and Her2, respectively.

XX SQ Sequence 1255 AA;  
 Query Match 96.3%; Score 4892; DB 21; Length 1255;  
 Best Local Similarity 73.1%; Pred. No. 0;  
 Matches 918; Conservative 0; Mismatches 1; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLALLPPGAASQVCTGTDMLRLPASPEHLDMLRLHYLQGVQVQGNL 60  
 DB 1 MELAALCRWGLLALLPPGAASQVCTGTDMLRLPASPEHLDMLRLHYLQGVQVQGNL 60  
 QY 61 ELTYLPTNASLSFLQDIQEVQGVYLIHQNQVQVPLQRLRVRGTQLFEDNYALAVLDNG 120  
 DB 61 ELTYLPTNASLSFLQDIQEVQGVYLIHQNQVQVPLQRLRVRGTQLFEDNYALAVLDNG 120  
 QY 121 DPLNNTTPTVGTGASPGRLQRLSLTEILKGGVLIQRLNQLCYQDTILMKDIFPKNNOLA 180  
 DB 121 DPLNNTTPTVGTGASPGRLQRLSLTEILKGGVLIQRLNQLCYQDTILMKDIFPKNNOLA 180  
 QY 181 LTLIDNRSRACHPCSPMKGSRGWGESSEDCQSLTRTVCAGGCARCKGFLPTDCCHEQC 240  
 DB 181 LTLIDNRSRACHPCSPMKGSRGWGESSEDCQSLTRTVCAGGCARCKGFLPTDCCHEQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 XX

Db 241 AAGCTGPKHSDCLACLFHNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLRVRVTSAN 360  
 Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLRVRVTSAN 360  
 QY 361 IOEFAGCKKIFGSLAFLEPESFDGDPASNTAPLOEQLOVFETLEITGVLYISAMPDSL 420  
 Db 361 IOEFAGCKKIFGSLAFLEPESFDGDPASNTAPLOEQLOVFETLEITGVLYISAMPDSL 420  
 QY 421 DLSVFQNLQVIRGRILHNGAYSLTQGLGISWLGRLSRRELGSGLALIHNTLHCFVHTV 480  
 Db 421 DLSVFQNLQVIRGRILHNGAYSLTQGLGISWLGRLSRRELGSGLALIHNTLHCFVHTV 480  
 QY 481 PWDQLFRNPQALHTANRPEDECYGEGLACHQLCARGHGWGPGTQCVCNCSQFLRGQEC 540  
 Db 481 PWDQLFRNPQALHTANRPEDECYGEGLACHQLCARGHGWGPGTQCVCNCSQFLRGQEC 540  
 QY 541 VEECRVLQGLPREYVYNAHCLPCHPECPONGSVTCFGEADQCVACAHYKDPFCVARC 600  
 Db 541 VEECRVLQGLPREYVYNAHCLPCHPECPONGSVTCFGEADQCVACAHYKDPFCVARC 600  
 QY 601 PSYKPKDLSYMPKPFDEEGACQPCPINCTHSCVDLDDKGCAPARASPLTS----- 653  
 Db 601 PSYKPKDLSYMPKPFDEEGACQPCPINCTHSCVDLDDKGCAPARASPLTSIVSAVVG 660  
 QY 654 ----- 653  
 Db 661 ILLVVVLGVVGLIKRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
 QY 654 ----- 653  
 Db 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPVAIKVLRNTSPKANKEILDEAYVMAGVGP 780  
 QY 654 ----- 653  
 Db 781 YVSRLLGICLTSTVOLVTQLMPYGCLLDHVRNRRGLSQDLLNWCMTAKGMSYLEVDR 840  
 QY 654 ----- 653  
 Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKVPKIKWMALESILRRRT 900  
 QY 654 ----- 653  
 Db 901 HQSDVMSYGVTVWELMTFAKPYDGIIPAREIPDLLEKGERLPQPPICTIDVYMIWKCM 960  
 QY 654 ----- QNEDLGPASPLDSTFYRSLLLEDDDMGLDVA 684  
 Db 961 IDSECRPRRELVSFSEFMRWDPQRFVVIQNEEDLGPASPLDSTFYRSLLLEDDDMGLDVA 1020  
 QY 685 EBYLVPQOQFFCPDPAPGAGVMVHRHRSSTRSGGDLTLGLEPSEEBAPRSLAPSEG 744  
 Db 1021 EBYLVPQOQFFCPDPAPGAGVMVHRHRSSTRSGGDLTLGLEPSEEBAPRSLAPSEG 1080  
 QY 745 AGSDVFDGDLGMAAKGLQSLPHTDPSPLQRYSEBPTVPLPSETDGYVAPLTCSPQEV 804  
 Db 1081 AGSDVFDGDLGMAAKGLQSLPHTDPSPLQRYSEBPTVPLPSETDGYVAPLTCSPQEV 1140  
 QY 805 NQPDVVRPQPPSPREGPLPAARAGATLERPKTSLCKNGVVKDVFAGGAVENPEYLTQ 864  
 Db 1141 NQPDVVRPQPPSPREGPLPAARAGATLERPKTSLCKNGVVKDVFAGGAVENPEYLTQ 1200  
 QY 865 GGAAPQPPPPAFSPAFDNLVYWDQPPPERGAPSTFKGTPTAENPEYLGLDVFPV 919  
 Db 1201 GGAAPQPPPPAFSPAFDNLVYWDQPPPERGAPSTFKGTPTAENPEYLGLDVFPV 1255

RESULT 14  
 AAEL12130  
 ID AAEL12130 standard; Protein; 1255 AA.  
 XX  
 AC AAEL12130;  
 XX

DT 18-DEC-2001 (first entry)  
XX Human tyrosine kinase-type receptor, HER-2.  
DE Therapeutic compound; major histocompatibility complex; vaccine;  
XX antigenic peptide; MHC; immunoregulatory; immune response; HER-2;  
KW adoptive immunotherapy; anti-cancer; breast cancer antigen; APC;  
KW antigen presenting cell; human; tyrosine kinase-type receptor.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
FH 774..782  
FT /note= "Antigenic epitope"  
XX  
PN WO200168677-A2.  
XX  
PD 20-SEP-2001.  
XX  
XX 16-MAR-2001; 2001WO-US40328.  
PF  
XX 16-MAR-2000; 2000US-0527487.  
PR  
XX (GENZ ) GENZYME CORP.  
PA  
XX Nicolette CA;  
PI  
XX WPI; 2001-616284/71.  
DR N-PSDB; AAD19731.  
XX  
XX Novel synthetic therapeutic compound for inducing immune response and  
PT for use in adoptive immunotherapy, has enhanced binding to major  
PT histocompatibility molecules and enhanced immunoregulatory properties  
PT  
XX  
XX Claim 4; Page 63-67; 69pp; English.  
XX  
XX The invention relates to synthetic therapeutic compounds (antigenic  
CC peptides) with enhanced binding to major histocompatibility complex  
CC (MHC) molecules and enhanced immunoregulatory properties relative  
CC to their natural counterparts. Compounds of the invention are useful  
CC for inducing an immune response in a subject and for use in adoptive  
CC immunotherapy. They are useful as components of anti-cancer vaccines  
CC and to expand immune effector cells that are specific for cancers  
CC characterised by expression of the breast cancer antigen, HER-2.  
CC Polynucleotides that encode peptides of the invention are useful as  
CC hybridisation probes and as primers for the detection of genes of gene  
CC transcripts that are expressed in antigen presenting cells (APCs), to  
CC confirm transduction of polynucleotides into host cells. The present  
CC sequence is human tyrosine kinase-type receptor, HER-2. Compounds  
CC of the invention are designed based on the HER-2 antigenic peptide  
CC (774-782).  
XX  
SQ Sequence 1255 AA;  
  
Query Match 96.3%; Score 4892; DB 22; Length 1255;  
Best Local Similarity 73.1%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 1; Indels 336; Gaps 1;  
  
QY 1 MELAAALCRWGLLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHYGQCQVQGNL 60  
DB 1 MELAAALCRWGLLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHYGQCQVQGNL 60  
QY 61 ELTYLPTNASLFLQDIOEVGYVLIHNOVROVPLQRLVRVGTOLFEEDNYALVLDNG 120  
DB 61 ELTYLPTNASLFLQDIOEVGYVLIHNOVROVPLQRLVRVGTOLFEEDNYALVLDNG 120  
QY 121 DPLNNTTVPVTCASPGGLRELOLRSLEILKGVLIQRPOLCYQDTILWKDIFHKNNOLA 180  
DB 121 DPLNNTTVPVTCASPGGLRELOLRSLEILKGVLIQRPOLCYQDTILWKDIFHKNNOLA 180  
QY 181 LTLIDTNRSRACHPCSPMCKGSRGWGESSEDCQSLTRTVGAGGCARCKGPLPTDCCHQC 240  
DB 181 LTLIDTNRSRACHPCSPMCKGSRGWGESSEDCQSLTRTVGAGGCARCKGPLPTDCCHQC 240

ID AAB60167 standard; Protein; 1255 AA.  
 AC AAB60167;  
 DT 03-APR-2001 (first entry)  
 DE HER2 transgene plasmid construct encoded protein.  
 XX  
 KW Human; HER2; ErbB2 receptor; p185neu; maytansinoid conjugate; cancer;  
 XX antibody.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200100244-A2.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-US17229.  
 XX  
 PR 25-JUN-1999; 99US-0141316.  
 PR 16-MAR-2000; 2000US-0189844.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Erickson S, Schwall R;  
 XX  
 DR WPI; 2001-061962/07.  
 DR N-PSDB; AAF24297.  
 XX  
 XX Treating tumors, particularly breast cancers, which overexpress an ErbB  
 PT receptor and does not respond to an anti-ErbB antibody, comprises  
 PT conjugating the antibody to a maytansinoid -  
 XX  
 PS Example 3; Fig 4; 92pp; English.  
 XX  
 CC The present invention provides a method of treating cancer by  
 CC administering a conjugate of anti-ErbB antibody with a maytansinoid. In  
 CC particular, the antibody is directed against ErbB2 (also known as HER2  
 CC and p185neu). The method is particularly useful in the treatment of  
 CC breast, ovarian, stomach, endometrial, salivary gland, lung, kidney,  
 CC colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.  
 XX  
 XX Sequence 1255 AA;  
 Query Match 96.3%; Score 4892; DB 22; Length 1255;  
 Best Local Similarity 73.1%; Pred. No. 0;  
 Matches 918; Conservative 0; Mismatches 1; Indels 336; Gaps 1;  
 QY 1 MELAALCRWGLLALPPGAASQVCTGTDMLRLPASPEHLDMRLHYQGCQVQGNL 60  
 DB 1 MELAALCRWGLLALPPGAASQVCTGTDMLRLPASPEHLDMRLHYQGCQVQGNL 60  
 QY 61 ELTYLPTNASLSFLQDIQEVQGVYLIHQNQVQVPLQRLIRVRGTQLPEDNYALAVLDNG 120  
 DB 61 ELTYLPTNASLSFLQDIQEVQGVYLIHQNQVQVPLQRLIRVRGTQLPEDNYALAVLDNG 120  
 QY 121 DPLNNTPTVTGASPGGLRELQRLSLTEILKGGVLIQRPOLCVQDTILMKDIFHKNQOLA 180  
 DB 121 DPLNNTPTVTGASPGGLRELQRLSLTEILKGGVLIQRPOLCVQDTILMKDIFHKNQOLA 180  
 QY 181 LTLIDNTRGRACHPCSPMKGSRCSWSESSEDOSLRTVTCAGGACRCKGLPTDCHEQC 240  
 DB 181 LTLIDNTRGRACHPCSPMKGSRCSWSESSEDOSLRTVTCAGGACRCKGLPTDCHEQC 240  
 QY 241 AAGCTGPKHSDCLACILFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 DB 241 AAGCTGPKHSDCLACILFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSPCARVCYGLGMEHLREVRVTSAN 360  
 DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSPCARVCYGLGMEHLREVRVTSAN 360

QY 361 IQEFAGCKKIFGSLAFLEPESFDGDPASNTAPLQEPQLOVFETLEBITGYLYISAMPDLSLP 420  
 DB 361 IQEFAGCKKIFGSLAFLEPESFDGDPASNTAPLQEPQLOVFETLEBITGYLYISAMPDLSLP 420  
 QY 421 DLSVFNQLOVIRGRILHNGAYSLTQGLGISWLGURSIRELGSGLALIHNNHLCFVHTV 480  
 DB 421 DLSVFNQLOVIRGRILHNGAYSLTQGLGISWLGURSIRELGSGLALIHNNHLCFVHTV 480  
 QY 481 PWDQLFRNPHQALLHTANRPEDECVEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQSC 540  
 DB 481 PWDQLFRNPHQALLHTANRPEDECVEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQSC 540  
 QY 541 VEECRVLQGLPREYVYNAHCLPCHPECPQNGSVTCFGEADQCACAHYKDPDFCVCARC 600  
 DB 541 VEECRVLQGLPREYVYNAHCLPCHPECPQNGSVTCFGEADQCACAHYKDPDFCVCARC 600  
 QY 601 PSGVKPDLSYMPIWKFPDEEGACQPCINCHTHSCVDLDDKGCPCAFORASPLTS----- 653  
 DB 601 PSGVKPDLSYMPIWKFPDEEGACQPCINCHTHSCVDLDDKGCPCAFORASPLTS----- 653  
 QY 654 ----- 653  
 DB 661 ILLVVVLGVVFGILLIKRRQOKIRKYTMERLLQETELVEPLTPSGAMPNQAOIRILKETEL 720  
 QY 654 ----- 653  
 DB 721 RKVKVLGSGAGTVYKGIWIPDGENVKIPVAIKVLRNTPSKANKEILDEAYVMAGVGSPP 780  
 QY 654 ----- 653  
 DB 781 YVSRLLGICLTSTVOLVTQMPYGLDHLVHNRGRGLSGQDILLNWMQIAKMSYLEVDR 840  
 QY 654 ----- 653  
 DB 841 LVHRDLAARNVLVKSFNHVKITDFGLARLLDIDETEHADGCKVKPIKMALESILRRRT 900  
 QY 654 ----- 653  
 DB 901 HQSDVMSYGVTVWELMTFGAKPYDGI PAEIPDLLEKGERLPQPPICTIDVYMIWVKWM 960  
 QY 654 -----ONEDLGPASPLDSTFYRSLLLEDDDDMDGLVDA 684  
 DB 961 IDSECRPRFRELVSFSEFARMARDPQRFVVIQNEDELGPASPLDSTFYRSLLLEDDDDMDGLVDA 1020  
 QY 685 BEYLVPQOGFFCPDPAAGAGWVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEB 744  
 DB 1021 BEYLVPQOGFFCPDPAAGAGWVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEB 1080  
 QY 745 AGSDVFDGDLGMAAKGLQSLPHTDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYV 804  
 DB 1081 AGSDVFDGDLGMAAKGLQSLPHTDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYV 1140  
 QY 805 NOPDYRPPPPSPREGPIPAARPAAGATLERPKTLSPGKNGVVKDVFAGGAVENPEYLTQ 864  
 DB 1141 NOPDYRPPPPSPREGPIPAARPAAGATLERPKTLSPGKNGVVKDVFAGGAVENPEYLTQ 1200  
 QY 865 GGAAPQPHPPPPAFSPAFDNLVYDQDPPERGAPPSTFKGTPTAENPEYLGLDVVP 919  
 DB 1201 GGAAPQPHPPPPAFSPAFDNLVYDQDPPERGAPPSTFKGTPTAENPEYLGLDVVP 1255

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 Job time : 59.6401 secs